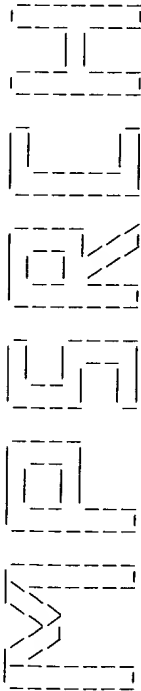


\*\*\*\*\*



(TM)

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPSrch\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:52:39 1999; MasPar time 25.13 Seconds  
390.202 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-026-400-2  
Description: (1-461) from US09026400.1.pap  
Perfect Score: 3223  
Sequence: 1 MVHQSNHGHEAAAAANGKS.....LERVKFCQRNKKNSINGC 461

Scoring table: PAM 150  
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 35.539; Variance 164.075; scale 0.217

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description	Pred. No.
1	3223	100.0	461	34	Nicotianamine aminotr	4.56e-283
2	2888	89.6	551	34	Nicotianamine aminotr	7.13e-252
3	403	12.5	394	26	Aquifex aspartate ami	8.25e-24
4	277	8.6	373	26	Aquifex aspartate ami	4.95e-13
5	276	8.6	398	26	Ammonifex degensii as	6.00e-13
6	231	7.2	482	26	Barley alanine aminot	3.19e-09
7	222	6.9	517	20	Carnation ACC synthas	1.73e-08
8	216	6.7	422	17	Human kynurenine amin	5.30e-08
9	209	6.5	423	17	Rat kynurenine aminot	1.95e-07
10	209	6.5	437	17	Rat kynurenine aminot	1.95e-07
11	209	6.5	457	17	Rat kynurenine aminot	1.95e-07
12	195	6.1	496	7	Rat ALR.	2.57e-06
13	180	5.6	480	32	Rose 1-aminocycloprop	3.93e-05
14	179	5.6	493	5	ACC synthetase.	4.71e-05
15	178	5.5	486	23	Poplar 1-aminocyclopr	5.64e-05
16	178	5.5	493	3	Zucchini ACC synthase	5.64e-05

17	178	5.5	493	29	W47311	Zucchini ACC synthase	5.64e-05
18	177	5.5	493	29	W47310	Protein encoded by zu	6.75e-05
19	177	5.5	493	3	R15504	Zucchini ACC synthase	6.75e-05
20	176	5.5	496	30	W46904	A human mutant alanin	8.08e-05
21	176	5.5	496	34	W62267	Modified human alanin	8.08e-05
22	175	5.4	493	7	R35230	Human ALR.	9.66e-05
23	169	5.2	362	20	W04559	Carnation ACC synthas	2.83e-04
24	166	5.2	494	29	W47312	Zucchini ACC synthase	4.82e-04
25	166	5.2	494	3	R15863	Zucchini ACC synthase	4.82e-04
26	165	5.1	469	3	R15510	Tomato ACC synthase e	5.75e-04
27	157	4.9	323	29	W37444	1-aminocyclopropane-1	2.36e-03
28	155	4.8	359	14	R72715	hisc gene product of	3.35e-03
29	148	4.6	363	26	W24256	Ammonifex histidinol-	1.13e-02
30	145	4.5	481	23	W21754	Poplar 1-aminocyclopr	1.90e-02
31	146	4.5	482	32	W60233	Pelargonium 1-aminocy	1.60e-02
32	146	4.5	482	32	W60234	Pelargonium 1-aminocy	1.60e-02
33	138	4.3	496	10	R53114	Crucifer 1-aminocyclo	6.29e-02
34	136	4.2	414	26	W24248	Aquifex aspartate tra	8.83e-02
35	135	4.2	485	3	R15507	Tomato ACC synthase e	1.05e-01
36	135	4.2	485	28	W34222	ACC synthase protein.	1.05e-01
37	135	4.2	485	29	W47314	Tomato ACC synthase L	1.05e-01
38	134	4.2	487	31	W57484	Papaya ACC synthase e	1.24e-01
39	133	4.1	390	22	W09879	ACC synthase GAC-2.	1.46e-01
40	133	4.1	485	3	R15506	Tomato ACC synthase e	1.46e-01
41	133	4.1	485	29	W47313	Tomato ACC synthase.	1.46e-01
42	125	3.9	330	19	R98599	Broccoli ACC synthase	5.56e-01
43	127	3.9	333	3	R13494	P.denitrificans COB C	3.99e-01
44	125	3.9	374	19	R98598	Broccoli ACC synthase	5.56e-01
45	125	3.9	490	32	W60235	Pelargonium 1-aminocy	5.56e-01

ALIGNMENTS

RESULT 1  
ID W61642 standard; Protein; 461 AA.  
AC W61642;  
DT 27-OCT-1998 (first entry)  
DE Nicotianamine aminotransferase 49564.15 molecular weight protein.  
KW nicotianamine aminotransferase; plant; iron absorption;  
OS iron deficiency chlorosis.  
FN Gramineae sp.  
PN EP-860499-A2.  
PD 26-AUG-1998.  
PF 19-FEB-1998; 102891.  
PR 21-FEB-1997; JP-037499.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
PI Mori S; Nakanishi H; Takahashi M;  
DR WPI; 98-439341/38.  
DR N-PSDB; W48147.  
PT New nicotianamine aminotransferase protein and DNA - useful for  
enhancing iron absorption of plant cells  
PS Claim 3; page 12-13; 17pp; English.  
CC The nicotianamine aminotransferase can be used in a plasmid to transform  
plant cells to produce cells with enhanced iron absorption, and it is  
implied [though not stated] that plants with improved resistance to iron  
deficiency chlorosis in calcareous soils can be regenerated from the  
transformed cells. The gene fragment can be used to detect, amplify  
and/or isolate nicotianamine aminotransferase genes.  
SQ Sequence 461 AA;

Query Match 100.0%; Score 3223; DB 34; Length 461;  
Best Local Similarity 100.0%; Pred. No. 4.56e-283;  
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvhqsngheaaaaaangksnghaaangksnghaaavaevnfargkdglattgaks 60

QY 1 MVHQSNHGHEAAAAANGKSNHAAAAANGSNHAAAAANGVFNFAFGKDGILLATTGAKNS 60

Db 61 irairyxisavveesgrrpvlplahqpsvfpafirtaveaedavaaalrtgqfncyaav 120

QY 61 IRAIRYKISAVSEESGRRPVLPLAHGDPVFPFRTAVEAEDAVAAALRTGQFNCYAGV 120

Db 121 glpaarsavaehlsqgvyklsaddvfltaggtqaleivlpiaqtaganillprpypn 180

QY 121 GLPAARSAVAEHLGSGVYKLSADDDVLTAGTQAEVLIIPVLAQTAGANILLPRGYPN 180  
 Db 181 yearaafnklevrfdltpdkgweididslesiadknttamvlnpnpcgsvsydydla 240  
 QY 181 YEARAFAFNKLEVRHFDLTPDKGWEIDIDSLESIAADKNTTAMVLIIPNPNPCGSVSYDYDHLA 240  
 Db 241 kvaevarklgilviadevygkvlgsapfipmgvfhgiapvlsglsksvlpwgrlgw 300  
 QY 241 KVAEARKLGILVIADEVYKVLGSAPFIPMGVFGHIAPIVLSGLSKSVLPVPGWRLGW 300  
 Db 301 vavydptkilektkistsitnlnvstddpatfvqealpkilntkadvfkriigllkess 360  
 QY 301 VAVYDPTKILEKTKISTITNVLNVDTPATFVQEALPKILENTKADTFKRIIGLLKESS 360  
 Db 361 eicyreikenkyitophkpegsmfvmvknlnllleehddidfccklakeesvilpcgsv 420  
 QY 361 EICYREIKENKYITCPHKPEGSMFVMVKNLNLHLEEHDDIDFCCKLAKEESVILPCGSV 420  
 Db 421 lgnmenvritfacvpslqdglervksfcgrnkknsingc 461  
 QY 421 LGMENVVRITFACVPSSLQDGLERVKSCQRNKKNSINGC 461

RESULT 2  
 ID W61643 standard; Protein; 551 AA.  
 AC W61643;  
 DT 27-OCT-1998 (first entry)  
 DE Nicotianamine aminotransferase 58148.62 molecular weight protein.  
 KW Nicotianamine aminotransferase; plant; iron absorption;  
 OS Gramineae sp.  
 PN EP-860499-A2.  
 PD 26-AUG-1998.  
 PF 19-FEB-1998; 102891.  
 PR 21-FEB-1997; JP-037499.  
 PA (SUMO) SUMITOMO CHEM CO LTD.  
 PI Mori S, Nakanishi H, Takahashi M;  
 DR WPI: 98-439341/38.  
 DR N-PSDB; V48148.  
 PT New nicotianamine aminotransferase protein and DNA - useful for  
 enhancing iron absorption of plant cells  
 PS Claim 3; Page 14-15; 17pp; English.  
 CC The nicotianamine aminotransferase can be used in a plasmid to transform  
 plant cells to produce cells with enhanced iron absorption, and it is  
 implied [though not stated] that plants with improved resistance to iron  
 deficiency chlorosis in calcareous soils can be regenerated from the  
 CC transformed cells. The gene fragment can be used to detect, amplify  
 and/or isolate nicotianamine aminotransferase genes.  
 SQ Sequence 551 AA;

Query Match 89.6%; Score 2888; DB 34; Length 551;  
 Best Local Similarity 88.1%; Pred. No. 7.13e-252;  
 Matches 409; Conservative 30; Mismatches 20; Indels 5; Gaps 1;  
 Db 88 resnghaeaadngesnehaedaaesngshaaaeaeveefnagdkdvglaatga 147  
 QY 3 HQSNGHEAAAAAANGKSNHAAAAANGKSNHAAAAA- - - - -VEWNEFARGKDGILATGA 57  
 Db 148 nmsirairyikisavqekgrprvplahgdpvfpafirtaveadaavaavrtggfncyp 207  
 QY 58 KNSIRAIRYIKISAVESGPRVPLAHGDPVFPFARTAVEADAVALAARLTQGFNCYA 117  
 Db 208 agvqlpaarsavaehlsqgypymlsaddvftagdtgaievliplvtaqtaganillprpg 267  
 QY 118 AGVQLPAARSAVAEHLGSGVYKLSADDDVLTAGTQAEVLIIPVLAQTAGANILLPRPG 177  
 Db 268 ypnyearaafnrlvrhfdltpdkgweididslesiadknttamvlnpnpcgsvsydyd 327  
 QY 178 YPNYEARAFAFNKLEVRHFDLTPDKGWEIDIDSLESIAADKNTTAMVLIIPNPNPCGSVSYDYD 237  
 Db 328 hlskvaevarklgilviadevygkvlgsapfipmgvfhgiapvlsglsksvlpwgr 387

QY 238 HLAKVAEARKLGILVIADEVYKVLGSAPFIPMGVFGHIAPIVLSGLSKSVLPQWR 297  
 Db 388 lgvavvydprkilcetkistsitnlnvstddpatfvqealpkilntkadvfkriigllk 447  
 QY 298 LGWAVYDPTKILEKTKISTITNVLNVDTPATFVQEALPKILENTKADTFKRIIGLLK 357  
 Db 448 esseicygkikenkyitophkpegsmfvmvknlnllleehddidfccklakeesvilcp 507  
 QY 358 ESSEICYREIKENKYITCPHKPEGSMFVMVKNLNLHLEEHDDIDFCCKLAKEESVILCP 417  
 Db 508 gsvlgmanvritfacvpslqdglervksfcgrnkknsingc 551  
 QY 418 GSVILGMENVVRITFACVPSSLQDGLERVKSCQRNKKNSINGC 461

RESULT 3  
 ID W24257 standard; Protein; 394 AA.  
 AC W24257;  
 DT 18-FEB-1998 (first entry)  
 DE Aquifex aspartate aminotransferase VF5/AA.  
 KW Aspartate aminotransferase; VF5/AA; chiral compound.  
 OS Aquifex sp. strain VF5.  
 PN WO9729187-A1.  
 PD 14-AUG-1997.  
 PF 21-JAN-1997; U01094.  
 PR 08-MAY-1996; US-646590.  
 PR 09-FEB-1996; US-599171.  
 PA (RECO-) RECOMBINANT BIOCATALYSIS INC.  
 PI Swanson RV, Warren PV;  
 DR WPI: 97-415343/38.  
 DR N-PSDB; T78781.  
 PT New transaminase(s) and aminotransferase(s) derived from host cells  
 PT - used for producing enzymes, and hybridisation probes for a cDNA or  
 genomic library  
 PS Claim 19; Fig 10; 95pp; English.  
 CC This protein sequence comprises aspartate aminotransferase VF5/AA  
 of Aquifex VF5, a strictly chemolithoautotrophic marine eubacterium  
 CC which grows optimally at 85-90 deg C and pH 6.8 in high salt  
 CC medium. The VF5/AA amino acid sequence was deduced from genomic  
 CC DNA (see J78781). Claimed thermostable transaminases and  
 CC aminotransferases (W24248-57) can be produced from native or  
 CC recombinant host cells for use with L- and/or D-amino acids for  
 CC production of optically pure chiral compounds used in the  
 CC pharmaceutical, agricultural and other industries. A method is  
 CC claimed for transferring an amino group from an amino acid to an  
 CC alpha-keto acid using a claimed enzyme. The measurement of  
 CC aspartate aminotransferase levels in blood serum is used as an  
 CC indicator of heart damage.  
 SQ Sequence 394 AA;

Query Match 12.5%; Score 403; DB 26; Length 394;  
 Best Local Similarity 29.1%; Pred. No. 8.25e-24;  
 Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;  
 Db 42 pdfdtpdfikeaciralregtkk-vapsagibelreaiaekllkenkveyk-pseiv-vs 98  
 QY 92 PAPRTAVEADEAVALAALRGQNCYAGVGLPAARSAVAEHL-SQG-VPYKLSADDDVLT 149  
 Db 99 agakmvlifmailde--gdevllpspywtytpeqirfggvpv-evplkkekgfqlsl 155  
 QY 150 AGGTQAI-EVLIIPVLAQTAGANILLPRPGVNYEARAAAF-NKLEVRHFDLTPDKGWEIDI 207  
 Db 156 edvkekvter-tkaivinspnptgavveeeekkkiaefcverqifiidecyeyfyvgd 214  
 QY 208 DSL-ESIAADKNTTAMVLIIPNPNPCGSVSYDYDLAKVAEARKLGILVIADEVYKVLGS 266  
 Db 215 akfvspsasdevknitftvnafsksysmtgwrigvva-c-peey-akv-ia-slns-qs 268  
 QY 267 APIPVGVEGH-TAPV-LSIGSLSKSVIIPVGLWGVAVYDPTKILEKTKISTITNVLN 324  
 Db 269 vs-nvttfaqygal-ealknpkdkdfvnmnaferrrdtaveelskipgmdivv-kpega 325  
 QY 325 VSTDPTATFVQ-EALPKILENTKA-DFFKRIIGLLKESSEICYREIKENKYITCPHKPEGS 382



biosynthesis in the plant. Its amino acid sequence was deduced from a full-length gene (T3896). Expression of a nucleic acid (T3897) coding for a fragment (W04559) of the ACC synthase in transgenic carnation reduces the formation of ACC synthase by co-suppression. The reduction in ACC synthase activity results in decreased climacteric ethylene prodn. by the plant and hence delayed senescence of flowers and buds after cutting, and increased post-harvest life.

Query Match 6.9%; Score 222; DB 20; Length 517;  
Best Local Similarity 27.4%; Pred. No. 1.73e+08;  
Matches 98; Conservative 91; Mismatches 136; Indels 33; Gaps 30;

D b 96 glpefrsavakfmgkardekvi fndprvmvsgasasetllfc lan-pgdaf lipspyp 154  
||| ||||| ||||| :  
Q y 121 GLPAARSAVAEHLISQGVPYKLSAD-DVFLTAGQTAEVIPVLAQTAGANILLPRPGY 179  
::  
D b 155 afnrldrlwrtgvnlipftcossnnfkikaealsayedalknikvkgiivntpsnplgt 214  
::  
Q y 180 NYEARAFNK-LEVRHFDLPDKGEWDIDSLSEI-AD---KNTAM-VII-NPNNPCGS 232  
::  
D b 215 vldkdtlkmlltfvnak-nhlhvcdelyattvfnspsfsisvaeivdkmhvngdlwhily 273  
||| ||||| ||||| :  
Q y 233 VYSYDLAKVAE-VARKLGIIVIADEVYGLVLGSPAPIPMG-VF-G--HIAPVLS-IG- 285  
::  
D b 274 slskdmqmpgfrvgiiysyn-drvvstarmmsaf-g-l-vssg-tgfmi aaallddddfr 328  
||| ||||| ||||| :  
Q y 286 SLKSNIWIPGRLGWAVDPDTKILETKITSTINTLVNSTDPATFVQALPKILENTK 345  
::  
D b 329 r-fivesrdlrfrhqht-sel-akigigclg-gnaalfwmldr-hlld eatverelk 383  
||| ||||| ||||| :  
Q y 346 ADFEKRIIG-LLESSEICREIKENKYITCPHKPEGSMFVMVKLNHLLEIEIH-D-DID 402  
::  
D b 384 lwrvinekvinspgsfscsepgwfrvcfamdnatldvalnirsrtrgvnds 441  
:  
Q y 403 FCCILAKEESVILCPGSV-LGME-NWYRITFACVP-SSLQDGUERVKSFQCRNKKNS 457

RESULT 8  
ID R89906 standard; Protein; 422 AA.  
AC R89906;  
DE 15-JUL-1996 (first entry)  
DE Human kynurenine aminotransferase (KAT).  
KW Kynurenine aminotransferase; KAT; Kynurenic acid; KYNA; kynurenine;  
KW KYN; brain; NMDA receptor; glutamatergic function.  
OS Homo sapiens.  
PN W09601893-A1.  
PD 25-JUN-1996.  
PF 23-JAN-1995; U07855.  
PR 07-JUL-1994; US-271667.  
PA (PHAA ) PHARMACIA SPA.  
PA (UYMA-) UNIV MARYLAND BALTIMORE.  
PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;  
PI Speciale C;  
PI WPI: 96-097623/10.  
DR N-PSDB; T11744.  
PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) -  
PT useful in gene therapy applications and for identifying KAT in brain  
PT tissue  
PS Example 4: Figure 4: Sipp; English.  
CC Sequences encoding Kynurenine aminotransferase (KAT) can be inserted  
CC into vectors and subsequently cells and hence can be used for gene  
CC therapy. The vector and host cells can be used for cerebral  
CC implantation to where KAT can directly catalyse the production of  
CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts  
CC as a negative endogenous modulator of cerebral glutamatergic  
CC function. KYNA concentrations and the activity of KAT show an  
CC increase with age. KAT inhibitors, by providing an increase of the  
CC glutamatergic tone at the NMDA receptor, could be useful in  
CC situations where NMDA receptor function is insufficient and/or KAT  
CC activity and KYNA levels are abnormally enhanced. Hence they could  
CC be particularly useful in the treatment of the pathological

Rat kynurenine aminotransferase (KAT) clone.  
KW Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;  
KN brain; NMDA receptor; glutamatergic function.  
OS Rattus rattus.  
PN WO9601893-A1.  
PD 25-JAN-1996.  
PF 23-JUN-1995; U07855.  
PR 07-JUL-1994; US-271667.  
PA (PHAA ) PHARMACIA SPA.  
PY (UYMA ) UNIV MARYLAND BALTIMORE.  
PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;  
PT Speciale C;  
DR WPI: 96-097623/10.  
N-PSDB; T11742.  
PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT)  
PT useful in gene therapy applications and for identifying KAT in brain  
PT tissue

Claim 16; Figure 3; 5lpp; English.

Sequences encoding kynurenine aminotransferase (KAT) can be inserted  
CC into vectors and subsequently cells and hence can be used for gene  
CC therapy. The vector and host cells can be used for cerebral  
CC implantation to where KAT can directly catalyse the production of  
CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts  
CC as a negative endogenous modulator of cerebral glutamatergic  
CC function. KYNA concentrations and the activity of KAT show an  
CC increase with age. KAT inhibitors, by providing an increase of the  
CC glutamatergic tone at the NMDA receptor, could be useful in  
CC situations where NMDA receptor function is insufficient and/or KAT  
CC activity and KYNA levels are abnormally enhanced. Hence they could  
CC be particularly useful in the treatment of the pathological  
CC consequences associated with the aging processes in the brain.  
CC Three KAT clones are described in T11560, T11742-43.  
SQ Sequence 437 AA;

Query Match                6.5%; Score 209; DB 17; Length 437;  
Best Local Similarity      33.0%; Pred.No. 1.95e-07;  
Matches     35; Conservative    24; Mismatches 46; Indels    1; Gaps

Db    168 lgsandwqlpaelaskftprtkvlnitpnmpglqkfyrmelvelnclcgqhddvcisd 273  
QY    197 LPDKGWEIDISLSIADKNTAMVINPNNPCGSVYSVDHLAKVAEVARKILGILVIAD 259  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
|| || :  
228 evyqgwlvghdhvsialpgmwdrtlitigsagksfsatgkwgvw 273  
QY    257 EVYGKLVLGFAPFMVGFGHI-APVLISIGLSKSWIWPGWRGLGW 301  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT    11

ID R89998 standard; Protein; 457 AA.  
AC R89998;  
DT 14-JUL-1996 (first entry)  
DE Rat kynurenine aminotransferase (KAT) clone.  
KW Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;  
KN brain; NMDA receptor; glutamatergic function.  
OS Rattus rattus.  
PN WO9601893-A1.  
PD 25-JAN-1996.  
PF 23-JUN-1995; U07855.  
PR 07-JUL-1994; US-271667.  
PA (PHAA ) PHARMACIA SPA.  
PY (UYMA ) UNIV MARYLAND BALTIMORE.  
PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;  
PT Speciale C;  
DR WPI: 96-097623/10.  
N-PSDB; T11743.  
PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT)  
PT useful in gene therapy applications and for identifying KAT in brain  
PT tissue

Claim 16; Figure 4; 5lpp; English.

Sequences encoding kynurenine aminotransferase (KAT) can be inserted  
CC into vectors and subsequently cells and hence can be used for gene  
CC therapy. The vector and host cells can be used for cerebral  
CC implantation to where KAT can directly catalyse the production of

CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts  
 CC as a negative endogenous modulator of cerebral glutamatergic  
 CC function. KYNA concentrations and the activity of KAT show an  
 CC increase with age. KAT inhibitors, by providing an increase of the  
 CC glutamatergic tone at the NMDA receptor, could be useful in  
 CC situations where NMDA receptor function is insufficient and/or KAT  
 CC activity and KYNA levels are abnormally enhanced. Hence they could  
 CC be particularly useful in the treatment of the pathological  
 CC consequences associated with the aging processes in the brain.  
 CC Three KAT clones are described in T11560, T11742-43.  
 CC Sequence 457 AA;

Query Match 6.5%; Score 209; DB 17; Length 457;  
 Best Local Similarity 33.0%; Pred. No. 1.95e-07;  
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;  
 Db 188 lpaandwldpaelaskftrtkvlnvntnnpplgkfvfmelelvancqhdvvcisd 247  
 QY 197 LIPDKGWEIDIDSLESIADKNTTAMVIINPNPFGSVYDHLAKVAEYARKLGILVIAD 256  
 Db 248 evyqvlvydghqhvslaslpqmwdrtrltlgsagksfsatgkwkvgw 293  
 QY 257 EYVGLVLSGSAFPMGVFGHI-APVLSIGSLKSWIVPGWLGWV 301

RESULT 12  
 ID R35231 standard; Protein; 496 AA.

AC R35231;  
 DT 10-AUG-1993 (first entry)  
 DE Rat ALT.  
 KW Primer; polymerase chain reaction; PCR; amplify; human; diagnosis;  
 KW alanine aminotransferase; ALT; marker; hepatic disease; serum.  
 OS Rattus rattus.  
 PN J05068548-A.  
 PD 23-MAR-1993.  
 PF 06-AUG-1991; 222318.  
 PR 06-AUG-1991; JP-222318.  
 PA (KAGA) KAGAKU OYOBI KESSEI RYOHO KENKYUSHO.  
 DR WPI: 93-136892/17.  
 DR N-PSDB: Q35231.  
 PT Human alanine-amino-transferase gene fragments - used as marker  
 PT in diagnosing hepatic diseases  
 PS Disclosure; Page 11-13; 15pp; Japanese.  
 CC The sequences given in R35230-31 represent human and rat alanine  
 CC aminotransferase (ALT) genes respectively. ALT is an important  
 CC marker in the diagnosis of hepatic disease. Gene fragments of ALT  
 CC can be used in inexpensive, large scale production of human ALT  
 CC which can then be used as a standard in the determination of human  
 CC serum ALT. See also Q40500-01.  
 CC Sequence 496 AA;

Query Match 6.1%; Score 195; DB 7; Length 496;  
 Best Local Similarity 29.2%; Pred. No. 2.57e-06;  
 Matches 45; Conservative 42; Mismatches 56; Indels 11; Gaps 9;  
 Db 123 ysisgqipredvagyierddgipadpnniflstgasdaivtmklilvsggeartgv 182  
 QY 116 YRAGVGLPAARSVAEHLISQ-GVPYKLSADDVFLTAGGTQAEIIVPLAQTAG-A-NI 171  
 Db 183 ltipypylpsaalaeldavqdyv-ldearavaldiaelrralcqardccprvlecin 241  
 QY 172 LLPRPGYPNFEAR-AAFNKLEVRHFDLPDKGWEIDIDSLE-SI--A-DKN-TTANVIIN 225  
 Db 242 pgnptqvqtrecieavirfafkegflfmadevy 275  
 QY 226 PNNPCSVSYDHLAKVAEYARKLGILVIADDEVY 259

RESULT 13  
 ID W60239 standard; Protein; 480 AA.  
 AC W60239;  
 DT 28-SEP-1998 (first entry)  
 DE Rose 1-aminocyclopropane-1-carboxylase synthase.

KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;  
 KW ethylene; transgenic plant; wilting; rose; pRosekacc7.  
 OS Rosa sp. cv. Red Cardinal.  
 PN W09814465-A1.  
 PD 09-APR-1998.  
 PF 30-SEP-1997; U17644.  
 PR 01-OCT-1996; US-724194.  
 PA (COLS ) UNIV COLORADO STATE RES FOUND.  
 PI Ranu RS;  
 DR WPI: 98-260994/23.  
 DR N-PSDB: V30330.  
 PT New isolated ACC synthase genes - are obtained from geranium and  
 PT rose, used to develop products for producing plants with reduced  
 PT ethylene levels, for increasing shelf-life  
 PS Claim 60; Fig 10; 77pp; English.  
 CC This amino acid sequence of this 1-aminocyclopropane-1-carboxylate  
 CC synthase (ACC synthase) of rose cv. Red Cardinal was deduced from  
 CC isolated cDNA clone pRosekacc7 (see V30330). The invention relates  
 CC to new isolated ACC synthase genes from geranium and rose (see  
 CC V30324-26 and V30330) and the use of antisense fragments of these  
 CC genes to control expression of ACC synthase genes in transgenic  
 CC plants, especially in geranium, rose and woody plants. By reducing  
 CC the amount of ACC synthase produced in plant cells, the rate of ACC  
 CC conversion to ethylene can be decreased. This can be used to  
 CC prolong the shelf-life of cut flowers and to reduce leaf yellowing  
 CC and petal abscission during shipping and storage.  
 CC Sequence 480 AA;

Query Match 5.6%; Score 180; DB 32; Length 480;  
 Best Local Similarity 27.0%; Pred. No. 3.93e-05;  
 Matches 48; Conservative 50; Mismatches 70; Indels 10; Gaps 7;  
 Db 120 geelgisgiacyqpsdglmeiklavagfmskaigsvtyvpsqivltagatpaieilsfc 179  
 QY 105 AAALRTGQFNCTAGAGVGLPAARSAVAEHLISQGVPKLS--ADDVFLTAGGTQAEIIVPV 162  
 Db 180 lads-gnaflpapyppgldrdvkwrtgvelipvpcrsadkfnlsitaldrafnagkkr 238  
 QY 163 LAQTAGANILLPRPGYPNFEARAFNK-LEVRHFDLPDKGWEIDIDSLE-SIAD-KNTT 219  
 Db 239 kvvrgiisnpsnpgsglltreslynlldfareknhhiisnelfagstyggseefvma 296  
 QY 220 AMV---II-NPNPCGSVYSYDHLAKVAEYARKLGILVIADDEVYKLVLSGSAFIPMG 273

RESULT 14  
 ID R25406 standard; Protein; 493 AA.  
 AC R25406;  
 DT 18-JAN-1993 (first entry)  
 DE ACC synthetase.  
 KW 1-aminocyclopropane-1-carboxylic acid synthetase; detriment;  
 KW ethylene; growth; maturity; aging; plant.  
 OS Cucurbita maxima.  
 PN J04169183-A.  
 PD 17-JUN-1992.  
 PR 31-OCT-1990; 296943.  
 PR 31-OCT-1990; JP-296943.  
 PA (SUMO ) SUMITOMO CHEM CO LTD.  
 DR WPI: 92-253389/31.  
 DR N-PSDB: Q25896.  
 PT Detriment induced ACC synthetase gene - used for control of  
 PT bio-synthesis of ethylene, for controlling growth, maturity and  
 PT ageing of higher plant  
 PS Claim 2; Fig 1; 10pp; Japanese.  
 CC The protein sequence was deduced from the DNA sequence of the gene  
 CC encoding detriment induced 1-aminocyclopropane-1-carboxylic acid  
 CC (ACC) synthetase (EC 4.4.1.14) which was obtcd. by screening a cDNA  
 CC library prepd. from cucurbita maxima mRNA. EC4.4.1.14 obtcd. from  
 CC cDNA library clones was screened by an antibody method to identify  
 CC colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.  
 CC Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene  
 CC controls the growth, maturing and aging of higher plants.  
 CC Sequence 493 AA;







\*\*\*\*\*

(TM)

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
 Copyright (c) 1993-1998 University of Edinburgh, U.K.  
 Distribution rights by Oxford Molecular Ltd

MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:50:56 1999; Waspar time 33.04 Seconds  
 761.473 Million cell updates/sec

Tabular output not generated.

Title: >US-09-026-400-2

Description: (1-461) from US09026400.pep

Perfect Score: 3223

Sequence: 1 MVHQSGHGEAAAAANGKS.....LVRKFCQKNKKNSG 461

Scoring table: PAM 150

Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrembl9

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 49.304; Variance 91.106; scale 0.541

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1275	39.6	389	10	049451 TYROSINE TRANSAMINASE-2.31e-248	
2	726	22.5	464	5	093703 F42D1.2 PROTEIN 1.33e-125	
3	495	15.4	429	2	033267 ASPARTATE AMINOTRANSFER 1.44e-75	
4	460	14.3	402	2	086587 PUTATIVE AMINOTRANSFER 3.71e-68	
5	439	13.6	401	1	059044 401AA LONG HYPOTHETICA 9.70e-64	
6	435	13.5	404	2	F71348 ASPARTATE AMINOTRANSFER 6.69e-63	
7	410	12.7	405	2	P77727 FROM BASES 2401667 TO 1.11e-57	
8	403	12.5	394	2	067781 ASPARTATE AMINOTRANSFER 3.15e-56	
9	401	12.4	402	2	088124 PUTATIVE AMINOTRANSFER 8.18e-56	
10	374	11.6	390	2	025383 SOLUTE-BINDING SIGNATU 3.08e-50	
11	368	11.4	357	2	005237 HYPOTHETICAL 39.5 KD P 5.20e-49	
12	365	11.3	397	2	050013 ASPARTATE AMINOTRANSFER 2.14e-48	
13	361	11.2	397	2	053870 PUTATIVE AMINOTRANSFER 1.41e-47	
14	342	10.6	382	2	054170 AMINOTRANSFERASE 1.03e-43	
15	330	10.2	391	1	058489 391AA LONG HYPOTHETICA 7.75e-41	
16	323	10.0	379	1	028151 ASPARTATE AMINOTRANSFER 7.02e-40	
17	299	9.3	389	1	059096 389AA LONG HYPOTHETICA 4.28e-35	
18	296	9.2	383	2	033822 ASPARTATE AMINOTRANSFER 1.88e-34	
19	295	9.2	385	2	056232 ASPARTATE AMINOTRANSFER 2.65e-34	
20	294	9.1	374	1	027916 ASPARTATE AMINOTRANSFER 4.17e-34	

21 290 9.0 390 1 038650 ASPARTATE AMINOTRANSFER 2.56e-33

22 283 8.8 400 2 086459 PUTATIVE ASPARTATE AMI 6.08e-32

23 277 8.6 373 2 065737 AMINOTRANSFERASE (ASPC 9.05e-31

24 268 8.3 432 1 038874 HYPOTHETICAL PROTEIN M 5.09e-29

25 263 8.2 389 2 055128 ASPARTATE AMINOTRANSFER 4.71e-28

26 261 8.1 418 5 021658 RO3A10.4 PROTEIN. 1.15e-27

27 259 8.0 371 2 053091 ORF. 2.78e-27

28 256 7.9 152 10 049450 HYPOTHETICAL 16.7 KD P 1.05e-26

29 256 7.8 373 1 035453 ASPARTATE AMINOTRANSFER 1.05e-26

30 250 7.8 373 1 030304 ASPARTATE AMINOTRANSFER 1.47e-25

31 249 7.7 383 2 031028 ASPARTATE AMINOTRANSFER 2.88e-25

32 242 7.5 401 1 P95957 AMINOTRANSFERASE. 4.89e-24

33 235 7.3 435 10 094113 ACC SYNTHASE. 1.02e-22

34 224 7.0 482 10 082443 ALANINE AMINOTRANSFERA 1.16e-20

35 225 7.0 518 10 043753 1-AMINOCYCLOPROPANE 1- 7.58e-21

36 216 6.7 388 2 P96847 HYPOTHETICAL 41.0 KD P 3.50e-19

37 216 6.7 422 4 Q15773 GLUTAMINE--PHENYLPIRUV 3.50e-19

38 208 6.5 390 2 053620 AMINOTRANSFERASE. 1.02e-17

39 208 6.5 457 11 008415 MULTIFUNCTIONAL AMINOT 1.02e-17

40 211 6.5 482 2 P96681 YDEF PROTEIN. 2.89e-18

41 207 6.4 465 2 P96663 YDEF PROTEIN. 1.55e-17

42 203 6.3 444 10 043756 1-AMINOCYCLOPROPANE-1- 8.23e-17

43 203 6.3 493 10 Q42668 1-AMINOCYCLOPROPANE-1- 8.23e-17

44 200 6.2 409 5 061103 HYPOTHETICAL 44.4 KD P 2.86e-16

45 200 6.2 497 5 061101 HYPOTHETICAL 55.0 KD P 2.86e-16

## ALIGNMENTS

RESULT 1  
 ID 049451 PRELIMINARY; PRT; 389 AA.  
 AC 049451;  
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
 DE TYROSINE TRANSAMINASE-LIKE PROTEIN (EC 2.6.1.5)  
 GN F2109.100.  
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; TRACHEOPHYTA;  
 OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;  
 OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BEVAN M., KOETTER P., HEMPEL S., ENTIAN K.-D., HOHEISEL J.,  
 RA MEMES H.W., MAYER K., SCHUELLER C.;  
 RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU ARABIDOPSIS SEQUENCING PROJECT;  
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- CATALYTIC ACTIVITY: L-TYROSINE + 2-OXOGLUTARATE =  
 CC 4-HYDROXYPHENYLPYRUVATE + L-GLUTAMATE.  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 DR EMBL; AL021749; E1250059; -;  
 KW TRANSFERASE; AMINOTRANSFERASE.  
 SQ SEQUENCE 389 AA; 43018 MW; D4ECD89F CRC32;

Query Match 39.6%; Score 1275; DB 10; Length 389;

Best Local Similarity 47.5%; Ref. No. 2.31e-248;

Matches 170; Conservative 89; Mismatches 93; Indels 6; Gaps 6;

16 TQODETDSVWF-RGSNA-AKASS-VTMGVIVYKVFDECSLDVKKPLPLAHDPSV 72

31 SNGHAAAAVFVFAKGGKILATGAKNSIRAIKYSASVEESGPRPVPLAHDPSV 90

73 YPCYRTSILVENAVDVLRSRGKSNYPGAAGILPARQAVADVNNRDLTNKVPNDVFTV 132

91 FPAFTAVEAEDAAVALRTGQFNCVACVGLPAARSVAEHLSSQGVPKLSADDDVFLTA 150

133 GCNQGLETVLQSLAR-PNANILLPRPSYPHYEARAVYSGLGVKFDLLPEKEWEIDLPGI 191

151 GGTQATIEVVIPLAQTAGANILLPRFGYPNYEARAAFNKLEVRHFDLIPDKGWEIDSL 210







```

RT "The complete genome of the hyperthermophilic bacterium Aquifex
RL aeolicus";
RN NATURE 392:353-358(1998).
RC SEQUENCE FROM N.A.
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.,
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE000766; G2984217;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 394 AA: 43777 MW; B9D83011 CRC32;

Query Match 12.5%; Score 403; DB 2; Length 394;
Best Local Similarity 29.1%; Pred. No. 3.15e-56;
Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;

Db 42 PFDTPDFKEACIRALREGTK-YAPSAGIPELREAIKELKENKVEYK-PSEIV-VS 98
QY 92 PAFRTAVEAEDAAVALRTGQFCYAAAGVGLPAARSAAEHL-SQG-VPYKLSADDDVFLT 149
Db 99 AGAKWVLELIEAALDE--GDEVLLSPYVWVYTPQIRFEGGVV-EVPLKKEKGQLSL 155
QY 150 AGTQAI-EVILPVLAQTAGANLLPRPGVYNEARAFAF-NKLEVRHFDLPDKGWEIDI 207
Db 156 EDVKERVTER-TRAIVINSPNPTGAVYEEELKIAEFCVERGFIIFISDECVEYFVGD 214
QY 208 DSL-ESIADKNTAMVLIINPNPCGVSVDYDLAKVAEYARKLGILVIADEVYKGLVLS 266
Db 215 AKFVSPASDSVKNITFTVAFPSKSYMTGNRIGTVA-C-PEEY-AKV-IA-SLNS-OS 268
QY 267 APFIPMGVFGH-IAPV-LSIGLSKSWIVPGWRLGVAVVDPTKILEKTKISTITNYLN 324
Db 269 VS-NVTTFAYQYAL-EALKNPKSKDVNEMRANAFERRRTAVEELSKIPGMDVV-KPEGA 325
QY 325 VETDPATFVQ-RALPKILENTRK-ADFFKRIIGLLKESSEICYEIKENKIYTCPHKPEGS 382
Db 326 FYIFPDPSAYA-EKLGDDVKLSEFLLEKAKVAVVPGAFGAFGFLRLSYALSEERLVEGI 384
QY 383 MFVMVKLNHLLEEIHDDIDFCKLAKEESVILCPGSLGMENWVRITACVPSSLODGL 442
Db 385 RIK 388
QY 443 ERVK 446

RESULT 9
ID 088124 PRELIMINARY; PRT; 402 AA.
AC 088124;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN STGA.
OS STREPTOMYCES ANULATUS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA TERCERO J.A., ESINOSA J.C., JIMENEZ A.;
RT "Stgr, a new Streptomyces alboniger member of the Lysr family of
RL transcribed regulatory regulators."
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ006517; E1318411;
DR EMBL: AJ005198; E1318407;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 402 AA: 44414 MW; 5CD3256A CRC32;

Query Match 12.4%; Score 401; DB 2; Length 402;
Best Local Similarity 26.7%; Pred. No. 8.18e-56;
Matches 97; Conservative 94; Mismatches 152; Indels 20; Gaps 17;

RT "The complete genome of the hyperthermophilic bacterium Aquifex
RL aeolicus";
RN NATURE 392:353-358(1998).
RC SEQUENCE FROM N.A.
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.,
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE000766; G2984217;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 394 AA: 43777 MW; B9D83011 CRC32;

Query Match 11.6%; Score 374; DB 2; Length 390;
Best Local Similarity 26.7%; Pred. No. 3.06e-50;
Matches 97; Conservative 85; Mismatches 158; Indels 23; Gaps 19;

Db 40 PFDTPQAIAKALNDG-FTKYTPVAGIPELLKATAFKLKENNLDYEPNEILVNSG 98
QY 92 PAFRTAVEAEDAAVALRTGQFCYAAAGVGLPAARSAAEHL-SQGVPYKLSADDDVFLTAG 151
Db 99 AKQSLFNAIOALIE-EGDEVIIPFVFWTYPELVKYSY-GVSQFIQTDEKSHFKITPKOL 156

```

```
QY 152 GTQAEVILPVLQAQTAGANILLPRGYPNYEARAFNKLEVRHFDLIPDKG-WEIDIDSL 210
Db 157 KDALSPK-TKMLILTPSPTGMLYSKALEVLGEVLKDTKVVWLSDEIYEKLYV-KGEF 214
QY 211 -ESIAKDNTAMVIINPNPCGSVSYDHLAKVAEYARKLGLVIADEYVGLVLSAPF 269
Db 215 VSCAAVSEEMKKRTITISGLSKSVAMTGRMGVAAASKKLVKLMNLSQCTSNINSIT 274
QY 270 IP-MGVFGHIA-PVLSIGLSKSWIVPGHRLGWAVYDFTKLETKISTSTYNLNVST 327
Db 275 QMASIVALEGLVDKEIETMRQAFERC-DL--AHAKI--NAI-GG--LN-ALGPDGAFLY 325
QY 328 DPATFVO-EAL-PKILENTKADFKRIIGLLKESSEICVREIKENKYITCPHKPEGSMEV 385
Db 326 FTHIG-SLCGG--DSMRFCHELLEKGVALVPCKAFLGEGYVRLSFACSEEEIEKGIERI 382
QY 386 MYKLNJHLLEIHDIDFCKLAKEESVILCPGSLVGMENWVRITFACVPSSLQDGLERV 445
Db 383 ARF 385
QY 446 KSF 448

RESULT 11
ID Q05237 PRELIMINARY; PRT: 357 AA.
AC Q05237;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 39.5 KD PROTEIN.
GN YUGH.
OS BACILLUS SUBTILIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA OUEGA B.; KONINGSTEYN G.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 1-214 FROM N.A.
RC STRAIN=168;
RA DANCHIN A.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA OUEGA B.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE; 98044033.
RA KUNST F., OGASAWARA N., MOSTER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOFIN A., BORCHERT S.,
RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,
RA GHIM S.X., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOISAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAWATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBATASHI Y., KOETTER P., KONINGSSTEIN S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., OUEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
RA PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
```

```
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SERIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKEUCHI M., TAKAKASHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL NATURE 390:249-256(1997).
RN [5]
RC SEQUENCE FROM N.A.
RC STRAIN=168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; Z93934; E311527; -.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
DR KW HYPOTHETICAL PROTEIN; PYRIDOXAL PHOSPHATE.
SQ SEQUENCE 357 AA; 39461 MW; FD6B02F9 CRC32;

Query Match 11.4%; Score 368; DB 2; Length 357;
Best Local Similarity 29.8%; Pred. No. 5,20e-49;
Matches 68; Conservative 59; Mismatches 83; Indels 9; Gaps 9;

Db 38 PDFVTAMNVRASILSLEQG-YTSTYANAGLYSLREEISRYLSNRFDSLVS-PDNEIIVT 95
QY 92 PAFTRAEDAEVAAALRTGQFNCAAGVGLPAARSVAEHL-S-Q-GVPYKLSADDDVLT 149
Db 96 VGASQALDIATRAIVN-PGEEVILPEPCFVADALVSLAGGIPV-HVHTADKDGKATPA 153
QY 150 AGGTQAEIIVIPVLAQTAGANTLLPRGYPNYEARAFNK-LEVRHFDLIPDKGWEIDID 208
Db 154 DFEAAVTEKTKAILICSPNPTGTSYVSKELNEIAEFAKKHVDVIVLADEIYAEIYDEP- 212
QY 209 SLESTADKNTTAMVIINPNPCGSVSYDHLAKVAEYARKLGLVIADEYVGLVLSAP 268
Db 213 FTSIALPGMKERTVVISGFSKAFAMTGWRLGFAA 247
QY 269 FIPMGVF-GHTAPVLSIGLSKSWIVPGWRLGWA 302

RESULT 12
ID Q60013 PRELIMINARY; PRT: 397 AA.
AC Q60013;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1).
GN AAT.
OS STREPTOMYCES VIRGINIAE.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIADAE;
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA KATAYAMA M., SAKAI Y., OKAMOTO S., IHARA F., NIHIRA T., YAMADA Y.;
RT "Gene organization in the ada-rpl region of the Streptomyces
RT virginiae chromosome."
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; D50624; D1009940; -.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
DR KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
SQ SEQUENCE 397 AA; 42381 MW; 9240ED06 CRC32;
```

```

Query Match      11.3%; Score 365; DB 2; Length 397;
Best Local Similarity 28.5%; Pred. No. 2.14e-48;
Matches 84; Conservative 76; Mismatches 118; Indels 17; Gaps 16;

Db 25 AGRPVGIFGAGPD-FPT-PDYI-VEAAVEAC-RNPKYHRYTPAGLPLKAAIAAKTL 80
QY 75 SGRPVLPLAHGDPSPFPFAFTAVEADAFAAALRTGTQFCNYAAGVGLPAARSAVAEHL 134

Db 81 RDSGEVEARSOVLVTNGKQAIYEAFAAIL-D-PGDEVIPAPYWTYTPESIRLAG-GVP 137
QY 135 QGVYKLSADDDVLTAGGTQAI-EVIPVLAQTAGANILLPRGYPNYEARAFAFNKLEVR 193

Db 138 -VDVADETTGYRVSVEOLEAARTERTKVVLVSPNSNPTSGSVSEADAKAIGWAHGL 196
QY 194 HFDLIPD--KGWEIDIDSLESIAKNTAMVINPNPCGSGSVSYSDHLAKVAEVARVKIGI 251

Db 197 WVLTDIEYHLVYGEAKFTSLPLVPLPALRDKCIIVNGVAKTYAMTGRVGVW-IAQDVI 255
QY 252 LVIADEVYGLVLSGAPFIPMGVFGH-I-APVLSIGLSKSWIPVGRWGVAVYDPTKI 309

Db 256 KAATINLQSHATSNVSNVAOVAALAAVSGNLDVAEMRKA-FDRRRQTMVKMLNEI 309
QY 310 LEXTKISTSTINVL-NVSTDPA-TFVQEALPKILENTKADFFRKRIIIGLLKESSEI 362

RESULT 13
ID O53870 PRELIMINARY; PRT; 397 AA.
AC O53870;
DT 01-JUN-1998 (TREMELREL. 06, CREATED)
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN MT043.51C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORINEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA HAMILIN N., CHURCHER C.M.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULET S., EIGLMETER K., PASCOPELIA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae."
RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR EMBL; AL022004; E1254000; -.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 397 AA; 42209 MW; 447498CB CRC32;

Query Match      11.2%; Score 361; DB 2; Length 397;
Best Local Similarity 30.9%; Pred. No. 1.41e-47;
Matches 68; Conservative 56; Mismatches 87; Indels 9; Gaps 9;

Db 57 YPPGCSAPLRRAIAQRHRRHFVDYD-PETEVLTIVTGATEAFAAAVGLVE-PGSEVLL 114
QY 116 YAAGVGLPAARSAVA-EHLSQ-GVPYKLSADDDVLTAGGTQAIETIIPVLAQTAGANILL 173

Db 115 IEPFYDSYSPVAVAGARHRTVPLVDGRGFALDADALRRVTPTRTRALIINSPHNTGCA 174
QY 174 PRGYPNYEARAFAFNKLEVRHFDLIPD-KGWEIDIDSLESIAKNTAMVINPNPCGS 232

```

```

Db 175 VLSATELAAIAEIAAANLWVITDEVYEHVLFDHARHLPLAGFDGMAERTITISSAAKMF 234
QY 233 VYSYDHLAKVAEVARVKILGILVIADEVYKLVLSAFAFIPMGVFGHIA-PVLSIGSLSKSW 291

Db 235 NCTGWKIGW-A-CGPAELIAGVRAAKOYLSYVGGAPFQPA 272
QY 292 IVPGRWLGWVAVYDPTKILEKTISTITNYLNVST-DPA 330

RESULT 14
ID O54170 PRELIMINARY; PRT; 382 AA.
AC O54170;
DT 01-JUN-1998 (TREMELREL. 06, CREATED)
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE AMINOTRANSFERASE.
GN SC7HL.11.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE; 97000351.
RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL MOL. MICROBIOL. 21:77-96(1996).
DR EMBL; AL021411; E1245740; -.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 382 AA; 40860 MW; 9FC8F75A CRC32;

Query Match      10.6%; Score 342; DB 2; Length 382;
Best Local Similarity 26.1%; Pred. No. 1.03e-43;
Matches 80; Conservative 83; Mismatches 131; Indels 13; Gaps 10;

Db 1 MIATPPASRIAEELRRSRPALAPPGAVSLAMGEPD-FPTPTVYQA--AVSA-LREG 56
QY 52 LATGTAKNSIRAIRYKISAVEESGPRVPLPLAHGDPSPVPAFTAVEADAFAAALRTG 111

Db 57 HPH-YADQGLRELRAALARPERRGGAWDADDVLVTHGATAAALAAV-LATVGPDRV 114
QY 112 QFNCTAAGVGLPAARSAVAEHLISQGVYKLSADDDVLTAGGTQAIETIIPVLAQTAGANI 171

Db 115 VYPEPAYSILYADLVLAGTGVFVPLAPLHW--DLDALAAALP-GAAMMIFSNPSNPTG 171
QY 172 LLPRGYPNYEARAFAFNKLEVRHFDLIPDKGWEIDIDSLESIAKNTAMVINPNPCG 231

Db 172 IVHREELKGLLDGTDVLVVSDEAYHRLAYPGHEPVSALEIESLRGTVYVOTFSKT 231
QY 232 SVYSYDHLAKVAEVARVKILVIADEVYKLV-LGSAFIPMGVFGHIAFVLSIGSLSKS 290

Db 232 YAMTGRVGYLI--GPREVLDAAQVHRTWNGSLNTAVOHAALALDLDGTVGAMADRY 289
QY 291 WIVPGWRLGWAVYDPTKILEKT-KISTSTINLYNVSTDPATFVQEPALPKILENTKADFF 349

Db 290 RORRDIV 296
QY 350 KRIIGLL 356

RESULT 15

```

```
ID O58489 PRELIMINARY; PRT; 391 AA.
AC O58489;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBREL. 09, LAST ANNOTATION UPDATE)
DE 391AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
GN PH0771.
OS PYROCOCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE; 98344137.
RA KAWARABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT "Complete Sequence and Gene Organization of the Genome of a
RT Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii Ot3.";
RL DNA RES 5:55-76(1998).
DR EMBL; AP000003; D1030806;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 391 AA; 44565 MW; A549ACDA CRC32;

Query Match 10.2%; Score 330; DB 1; Length 391;
Best Local Similarity 28.4%; Pred. No. 2.75e-41;
Matches 103; Conservative 82; Mismatches 148; Indels 30; Gaps 29;

Db 42 PDFTPKNIKEAAKRALDEG-WTHYTPNAGIPELREAVVEYKKFYGIDIEVENVIITAG 100
QY | | : : | | | | : : | | : : | | : : | | : : | | : : | | : : | |
92 PAERTAVEAEDAVAAALRTQFNCAAGVGLPAARGSAVAEHL SQGVYPYKLSADDDVELTAG 151
Db 101 AYEGTILAFESLLER-GDEVIIIPDPAFVSVAEDAKVAEAK-PVR-IPLRENNFLDPNE 157
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 GTOAIEVIIIPVLAOTAGANILLPRGYPNY-E-ARAFNKLVRHFDLIPDKGWEIDIDS 209
Db 158 LLEKIS-KNTR-MIVINYPNNPTGATLD-KELAKTIADIAEDYNIYILSDPEYEHFIYED 214
QY | | : : | | : : | | | | | | : : | | : : | | : : | | : : | | : :
210 L-ESIADKNTAMVIN-PNNPCGSVYSYDHLAK-VAEVARKLGILVIADDEVYKLVLS 266
Db 215 AKHYPMIKFAPENTILA-NSFSKTFAMTGWRLGFV-Y-APSQVI-K-EM-TKLHAYV-IG 267
QY | | : : | | : : | | : : | | | | | | : : | | : : | | : : | | : :
267 APFIPMGVFGHIAPLVLSIGSLSKSWIVPGWRLGWAVVDPTKILEKTISTITNLNVS 326
Db 268 -NVASFVQIAGIEAL-RS-EESNKAYEEMKKEYNERRKIVVRLKNMPGKVKPEKGFAY 324
QY : : | | | | | | : : : : : : : : : : : : : : : : : : : : : : : :
327 TDPATFVQEARLPKILENTKADFFKRIIGLKESESEICYEIKENKYITCPH-K-PEGSMF 384
Db 325 VFPNIS-G--TGMSSSE-KFSEWLLLEKARVVVPIPTAFGRMGEGYVRISYATSKELIEM 380
QY | : : : : : : : : | | : : | | : : | | : : | | : : | | : : | : :
385 VMVKLNHLLEEIHDDIDFCCKLAKESVILCPGSLV-G-M-ENWVRITFACVPSSIQDGL 442
Db 381 NRI 383
QY : | :
443 ERV 445
```

Search completed: Fri Oct 1 13:51:35 1999  
Job time : 39 secs.



\*\*\*\*\*

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:51:53 1999; MasPar time 22.78 Seconds  
Tabular output not generated. 810.770 Million cell updates/sec

Title: >US-09-026-400-2  
Description: (1-461) from US09026400.pep  
Perfect Score: 3223

Sequence: 1 MVHQSNGHGEAAAAANGKS.....LERVKSFQCRNKKKNSINGC 461

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir60

1.pir1 2.pir2 3.pir3 4.pir4

Statistics: Mean 49.862; Variance 105.736; scale 0.472

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	920	28.5	454	1	XNRTY	2.11e-146
2	914	28.4	454	2	tyrosine transaminase	3.08e-145
3	495	15.4	429	2	H70506	2.11e-65
4	439	13.6	401	2	D71003	4.22e-55
5	410	12.7	405	2	H65000	7.94e-50
6	403	12.5	394	2	A70469	1.47e-48
7	394	12.2	402	2	S07088	6.17e-47
8	376	11.7	390	2	H71909	1.05e-43
9	374	11.6	390	2	H64603	2.40e-43
10	368	11.4	357	2	G70010	2.83e-42
11	368	11.4	375	2	A64300	2.83e-42
12	361	11.2	397	2	B70815	5.00e-41
13	358	11.1	392	2	A38621	1.71e-40
14	330	10.2	391	2	E71125	1.50e-35
15	330	10.2	393	2	C69591	1.50e-35
16	323	10.0	379	2	A69516	2.52e-34
17	308	9.6	412	2	E71718	1.03e-31
18	299	9.3	389	2	E71009	3.69e-30
19	299	9.3	392	2	C69672	2.48e-30
20	300	9.3	592	2	SC4923	1.21e-29
21	296	9.2	383	2	JC5775	1.80e-29
22	295	9.2	385	2	JC4537	1.80e-29
23	294	9.1	374	2	G59119	2.68e-29

294 294 9.1 507 2 S52677 probable membrane pro 2.68e-29  
25 290 9.0 390 2 F69452 aspartate aminotransf 1.30e-28  
26 285 8.8 400 2 A47094 aspartate transaminas 9.33e-28  
27 277 8.6 373 2 E70338 aminotransferase (Asp 7.15e-26  
28 268 8.3 432 2 F64484 alanine transaminase 7.17e-25  
29 263 8.2 389 2 S74343 aspartate aminotransf 4.98e-24  
30 258 8.0 444 2 S56832 kynurenine aminotrans 3.43e-23  
31 256 7.9 389 2 S75949 hypothetical protein 7.41e-23  
32 250 7.8 373 2 F69545 aspartate aminotransf 7.39e-22  
33 242 7.5 401 2 S75385 probable aspartate tr 1.56e-20  
34 241 7.5 410 2 A40658 aspartate transaminas 2.28e-20  
35 235 7.3 386 2 F64793 ybdl protein - Escher 2.20e-19  
36 231 7.2 482 2 S42535 alanine transaminase 9.90e-19  
37 227 7.0 516 2 S19252 1-aminocyclopropane-1 4.42e-18  
38 225 7.0 518 2 S31442 1-aminocyclopropane-1 9.33e-18  
39 222 6.9 387 2 S32934 aminotransferase patB 2.85e-17  
40 221 6.9 399 2 S39740 aspartate aminotransf 4.13e-17  
41 216 6.7 388 2 C70605 probable aminotransfe 2.62e-16  
42 216 6.7 422 2 S52790 glutamine-phenylpyru 2.62e-16  
43 217 6.7 482 2 S38429 alanine transaminase 1.81e-16  
44 211 6.5 385 2 S8456 histidinol-phosphate 1.65e-15  
45 211 6.5 482 2 B69780 transcription regulat 1.65e-15

## ALIGNMENTS

RESULT 1

ENTRY XNRTY #type complete  
TITLE tyrosine transaminase (EC 2.6.1.5) - rat  
ALTERNATE\_NAMES tyrosine aminotransferase  
ORGANISM formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 26-Feb-1999

ACCESSIONS A23310; A31804; JN0343; A48430; S18308; S17849  
REFERENCE A23310  
#authors Grange, T.; Guenet, C.; Dietrich, J.B.; Chasserot, S.; Fromont, M.; Befort, N.; Jami, J.; Beck, G.; Pictet, R.  
#journal J. Mol. Biol. (1985) 184:347-350  
#title Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme.  
#cross-references MUID:85293103  
#accession A23310  
#molecule\_type mRNA  
#residues 1-454 #label GRA  
#cross-references EMBL:X02741; NID:957327; PID:957328  
#note part of this sequence was confirmed by protein sequencing

REFERENCE A31804  
#authors Hargrove, J.L.; Scoble, H.A.; Mathews, W.R.; Baumstark, B.R.; Biemann, K.  
#journal J. Biol. Chem. (1989) 264:45-53  
#title The structure of tyrosine aminotransferase. Evidence for domains involved in catalysis and enzyme turnover.  
#cross-references MUID:89079691  
#accession A31804  
#molecule\_type mRNA  
#residues 226-284, 'G', 286-358, 'DL', 361-444, 'D', 446-454 #label HAR  
#cross-references GB:M18340  
#note the authors translated the codon GGG for residue 285 as Pro  
#note part of this sequence was confirmed by protein sequencing

REFERENCE JN0343  
#authors Zelenin, S.M.; Popova, V.S.; Morozov, I.V.; Tishkav, V.I.; Egorov, A.M.; Mertvetsov, N.P.  
#journal Bioorg. Khim. (1991) 17:994-996  
#title Nucleotide sequence of an EcoRI-fragment of the rat tyrosine aminotransferase gene determined on the automated sequencer "Applied Biosystems" model 370A.  
#cross-references MUID:92172066  
#accession JN0343  
#molecule\_type DNA

```

##residues      385-454 ##label ZEL
##experimental_source liver
REFERENCE
#authors      Morozov, I.V.; Mishin, V.P.; Zelenin, S.M.; Popova, V.S.;
               Mertvetsov, N.P.
#journal      DNA Seq. (1990) 1:151-155
#title      Nucleotide sequence of rat liver tyrosine aminotransferase
               gene fragment.
#cross-references MUID:92190544
#accession      A48430
#molecule_type DNA
#status      preliminary
#residues      190-284,'L',286-386 ##label MOR
#cross-references GB:X15690; NID:957845; PID:g1334238
##experimental_source liver
##note      sequence extracted from NCBI backbone (NCBIN:89708,
               NCBIP:89709)
REFERENCE
#authors      Lorber, B.; Dietrich, J.B.; Kern, D.
               FEBS Lett. (1991) 291:345-349
#journal      Isolation and characterization of active N-terminal truncated
               apo- and holoenzyme of mammalian liver tyrosine
               aminotransferase.
#cross-references MUID:92038067
#accession      S18308
#molecule_type protein
#residues      38-52;58-81 ##label LOR
##experimental_source liver
REFERENCE
#authors      Dietrich, J.B.; Lorber, B.; Kern, D.
               Eur. J. Biochem. (1991) 201:399-407
#journal      Expression of mammalian tyrosine aminotransferase in
               Saccharomyces cerevisiae and Escherichia coli. Purification
               to homogeneity and characterization of the enzyme
               overproduced in the bacteria.
#cross-references MUID:92037592
#accession      S17849
#status      not compared with conceptual translation
#molecule_type DNA
#residues      1,'V',3-10 ##label DIE
##experimental_source liver
GENETICS
#introns      408/3
CLASSIFICATION #superfamily mammalian tyrosine aminotransferase
               acetylated amino end; aminotransferase; homodimer;
               phosphoprotein; pyridoxal phosphate
KEYWORDS
FEATURE
#region      383-394
               #region PEST sequence\
               #modified_site acetylated amino end (Met) #status
               experimental\
               #binding_site pyridoxal phosphate (Lys) (covalent)
               #status experimental
               #length 454 #molecular-weight 50635 #checksum 7044
SUMMARY
Query Match      28.5%; Score 920; DB 1; Length 454;
Best Local Similarity 34.3%; Pred. No. 2,11e-146;
Matches 137; Conservative 117; Mismatches 135; Indels 11; Gaps 10;

Db      49  SNKTFPIRAIVDNMKVQPNKTVISLISGDPVTFGNLPTDPEVTOAMKDALDSKGYNG 108
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57  AKNSIRAIRYKISA-SVEESGRPVLPPLAHGDPSPFPAPRTAVEADVAALRTGQFNC 115
Db      109  YAPSIGYLSRREVASVYHCHEAP--LEARDVILTSGCSQAIELCLAVLAN-PGONILIP 165
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
116  YAAGVGLPAARSAAVEHL-SQGVYPKLSADDDVFLTAGGTQAEIVIPVLAQTAGANILLP 174
Db      166  RGFSLYRLAESMGTEVKVLLNPKSWEIDKQLESIDETACLVVNNPSNPGSVF 225
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175  RPYGPNYEAFAFNKLEVRHFDLIPDKGWEIDIDSLEADKNKTATWIIINPNPCGSVY 234
Db      226  SKRHQKILAAERQCVPILADEIVGDMVFSCKYEPPLANLSNVPILSGGGLAKRWLPV 285
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235  SYDLAKVAEVRKGLGILVIADEVYKVLGSAFFIPMGVFGHIAFVLISIGLSLSKSWIYP 294

```

```

Db      286  GWRGLWILIHRRDIRGN-EIRDGLVKLSORILGPCTIVQGALKSIQRTPOPEFYHDTLS 344
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
295  GWRLGWVAVDPKILEKIKISTISINYNLNVSTDPATFVQEQALPKILENTKADFFKRIIG 354
Db      345  FLKSNADLCYCALAAIPGLQ-PVRPSGAMLYMGIEHMEHPPEFENDEVFETRLIAQAV- 402
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
355  LLKRESSICVREIKENKYITCPHKPEGSMEFVVKLNLHLLEIHHDDIDFCKLAKESVI 414
Db      403  HCLPAICFEPNFFRVVIT-VPEVMMLACSRIOECQEH 441
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415  LC-PGSVLGMENVRITFACVPSLSQ-DGLERVKSCQRN 452

RESULT      2
ENTRY      S10887      #type complete
TITLE      tyrosine transaminase (EC 2.6.1.5) - human
ALTERNATE_NAMES      tat; tyrosine aminotransferase
ORGANISM      #formal_name Homo sapiens #common_name man
DATE      04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
               08-Sep-1997
ACCESSIONS      S10887; S21425; S52087; S60718
REFERENCE      Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.
               Nucleic Acids Res. (1990) 18:3853-3861
               Isolation and characterization of the human tyrosine
               aminotransferase gene.
#cross-references MUID:90326506
#accession      S10887
#molecule_type DNA
#residues      1-454 ##label RET
#cross-references EMBL:X52509; NID:g36696; PID:e225804; PID:g1217965
REFERENCE      S21425
#authors      Serralini, G.E.; Breton, N.; Berube, D.; Gagne, R.; Labrie, F.
#submission      submitted to the EMBL Data Library, September 1990
#description      Nucleotide sequence of human tyrosine aminotransferase cDNA.
#accession      S21425
#molecule_type mRNA
#residues      1-454 ##label SER
#cross-references EMBL:X55675; NID:g37501; PID:g37502
REFERENCE      S52087
#authors      Serralini, G.E.; Luu-The, V.; Labrie, F.
#journal      Biochim. Biophys. Acta (1995) 1260:97-101
#title      Cloning and expression of human tyrosine aminotransferase
               cDNA.
#cross-references MUID:95092801
#accession      S52087
#status      preliminary
#molecule_type mRNA
#residues      1-454 ##label SE2
#cross-references EMBL:X55675; NID:g37501; PID:g37502
REFERENCE      S60718
#authors      Zelenin, S.M.; Mertvetsov, N.P.
#journal      Bioorg. Khim. (1994) 20:196-204
#title      Nucleotide sequence of human tyrosine aminotransferase gene.
#accession      S60718
#molecule_type DNA
#residues      1-454 ##label ZEL
GENETICS
#gene      GDB:TAT
#cross-references GDB:120398; OMIM:276600
#map_position      16q22.1-16q22.3
#introns      79/3; 114/1; 136/3; 189/3; 236/1; 253/3; 304/3; 347/3; 375/3;
               408/3
CLASSIFICATION #superfamily mammalian tyrosine aminotransferase
KEYWORDS      aminotransferase
SUMMARY      #length 454 #molecular-weight 50399 #checksum 6711
Query Match      28.4%; Score 914; DB 2; Length 454;
Best Local Similarity 33.6%; Pred. No. 3.08e-145;
Matches 134; Conservative 119; Mismatches 137; Indels 9; Gaps 9;

```

```

Db      49  AKKTFNPIRAIVDNMKVQPNKTVISLISGDPVTFGNLPTDPEVTOAMKDALDSKGYNG 108

```



```

QY 251 ILVIADEVYKVLGSAPIPMGVFGHIAPIVLSIGLSKSWIVPGWRLGWAVYDPTKIL 310
Db 262 SEVREAIKLAIRICPNTPGQFA--AIAG-LTGM-DYLKEYMKLKERDFIYKRLNE 317
QY 311 ETKTISTSTNVLNSTD-PATFVQEAALPKILENTKADFFKRIIGLLKESSEICYREIKE 369
Db 318 IFCIS-TTRQGAIFYIPRIE 337
QY 370 NKYITCPHKEGSMFVWVKLN 390

RESULT 5
ENTRY H65000 #type complete
TITLE hypothetical protein b2290 - Escherichia coli (strain K-12)
ORGANISM #formal_name Escherichia coli
DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997
ACCESSIONS H65000
REFERENCE A64720
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kiripatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references GB:AE000318; GB:U00096; NID:g1788623; PID:g1788627;
#accession H65000
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-405 #label BLAT
#cross-references GB:AE000318; GB:U00096; NID:g1788623; PID:g1788627;
#experimental_source strain K-12, substrain MG1655
#length 405 #molecular-weight 45517 #checksum 4760
SUMMARY
Query Match 12.7%; Score 410; DB 2; Length 405;
Best Local Similarity 27.3%; Pred. No. 7.94e-50;
Matches 100; Conservative 94; Mismatches 154; Indels 18; Gaps 18;
Db 17 IRGPVLEAKRLEEGNK-VLKNIGNPAPP-GFDAPDEILVDVIRNLTAQ-G-YCDSK 72
QY 61 IRAIRYKISAVEESGPRVPLAHGDPVFPPTAVEAEDAVAALRTGQFNCAAGV 120
Db 73 GLXSARKAIMQVQAGMR-DVTVEDIYIGNGVSELIVQAMQALLNS-GDEMLVPADYP 130
QY 121 GLPARSAVAEHL-SQGVYPKLSADDFLTAGGTQATEIIPVLAQTAGANILLPRGYP 179
Db 131 LWTAAVSLSSKAVHY-LCDESSWFPDLDIRAKITPRTRGVIINPNPTGAVYSKEL 189
QY 180 NYEARAAFNKLEVRHFLIPDKG-WEIDISLESIADKNTAMVIINPNPCGSVSYDH 238
Db 190 LMEIVEARQHNLIIFADEIYDKLYDDAEHSHIAPLAPDLLTIFENGSKTYRVAGFRQ 249
QY 239 LAKVAEVARKLGIIVIADEVYKVLGSAPIPMGVFGHIAPIVLSIGLSKSWIVPGWRL 298
Db 250 GWVYLNGPKK-HAKGYIEGLEMLASMRLCANVPQAQHAIQTLGGY-QSI-SEFTIPG-GR 305
QY 299 GWAVYDPTKILETKIST-SITVNLNSTD-PATF-VQEAALPKILENTKADFFKRIIGL 355
Db 306 LYEORNRWELINDIPGVSCV-KPGALYMPFKIDAKRFN-IHDDQKMLVDFLQEKVLL 363
QY 356 LKESSEICYREIKENKYITCPHKEGSMFVWVKLNHLLEIEHDDIDFCCCKLAKEESVIL 415
Db 364 VQGTAF 369
QY 416 CPGSVL 421

RESULT 6
ENTRY A70469 #type complete

```

```

TITLE aspartate aminotransferase - Aquifex aeolicus
ORGANISM #formal_name Aquifex aeolicus
DATE 08-May-1998 #sequence_revision 08-May-1998 #text_change
13-Sep-1998
ACCESSIONS A70469
REFERENCE A70300
#authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
#accession A70469
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-394 #label AOF
#cross-references GB:AE000766; NID:g2984216; PID:g2984217; GB:AE000657
#experimental_source strain VF5
GENETICS aspC1
#gene
CLASSIFICATION #superfamily aspartate transaminase
SUMMARY #length 394 #molecular-weight 43777 #checksum 8792
Query Match 12.5%; Score 403; DB 2; Length 394;
Best Local Similarity 29.1%; Pred. No. 1.47e-48;
Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;
Db 42 PDFDTPDFKEACIRALREGTK-YAPSAGIPELREAIKLLKENKYEK-PSEIV-VS 98
QY 92 PAFTAVEAEDAVAALRTGQFNCAAGVGLPAARSAVAEHL-SQG-VPYKLSADDFLT 149
Db 99 AGAKMVLFIIFMAILDE--GDEVLLPSPVWVYTPQIRFFGGVPV-EVPLKKEKGQLSL 155
QY 150 AGGTOAI-EVIIPVLAQTAGANILLPRGYPNYEARAAF-NKLEVRHFLIDPKGWEIDI 207
Db 156 EDVKEKVTET-KAIVINSNNPTGAVYEEELKKAIEFCVERGIFIISECYEYFVGD 214
QY 208 DSL-ESIAKNTAMVIINPNPCGSVYSYDLAKVAEYARKLGIIVIADEVYKVLG 266
Db 215 AKFVSPASFSEYKNITFTVNAFSKYSMTGWRIGVYA-C-PEEY-AKV-IA-SLNS-OS 268
QY 267 APIPMGVFGH-IAPV-LSIGLSKSWIVPGWRLGWAVYDPTKILETKISTITN 324
Db 269 VS-NVITFAQYGL-EALNPKSKDFVNMENRAFERRRTAVEELSIFQMDVV-PKEGA 325
QY 325 VSTDPTATFVQ-EALPKILENTKA-DFFKRIIGLLKESSEICYREIKENKYITCPH 382
Db 326 FYIFPDPSAVA-EKLGDDVKLSFELLEKAKVAVVPGSAFGAPGFLRLSYALSSE 384
QY 383 MFVWVKLNHLLEIEHDDIDFCCCKLAKEESVILCPGSLGMENWVITFACVPSS 442
Db 385 RRIK 388
QY 443 ERVK 446
RESULT 7
ENTRY S07088 #type complete
TITLE aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM #formal_name Sulfolobus solfataricus
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
13-Sep-1998
ACCESSIONS S07088; S27106; S45613
REFERENCE S07088
#authors Cubellis, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino,
G.; Sannia, G.
#journal Eur. J. Biochem. (1989) 186:375-381
#title Cloning and sequencing of the gene coding for aspartate
aminotransferase from the thermoacidophilic archaeobacterium

```

```
#cross-references MUID:90092126
#accession S07088
#molecule_type DNA
#residues 1-402 #label CUB
#cross-references EMBL:X15505; NID:g47497; PID:g809765
#accession S27106
#molecule_type protein
#residues 2-38:297-306:308-327:400-402 #label CU2
REFERENCE
#residues S45613
#authors Zappacosta, F.; Sanna, G.; Savoy, L.A.; Marino, G.; Pucci,
Eur. J. Biochem. (1994) 222:761-767
#journal
#title Post-translational modifications in aspartate
amino transferase from Sulfolobus solfataricus. Detection of
N-epsilon-methyllysines by mass spectrometry.
#cross-references MUID:94298815
#accession S45613
#status preliminary
#molecule_type DNA
#residues 2-402 #label ZAP
GENETICS
#start_codon GTG
#superfamily aspartate transaminase
#amino transferase
KEYWORDS
#length 402 #molecular-weight 45732 #checksum 791
Query Match 12.2%; Score 394; DB 2; Length 402;
Best Local Similarity 24.7%; Pred. No. 6.17e-47;
Matches 96; Conservative 118; Mismatches 153; Indels 22; Gaps 18;
Db 22 YKEIARNVEKKIKIDFGIGQDPL-PTFKR-IR--DAAKEALDQG-FTFYTSAFGIDE 76
QY 56 YK-ISAASVEESGPVPLANGDSVPFAFTAVEADAVALRTGQFNCYRAGVGLPA 124
Db 77 LREKIAQVNTRYGTDVKEEVVTPGAKPALFLV-ILYINPSEVILDPDPSPSYAEV 135
QY 125 ARSAVAEHLQGVYKLSADSVFTAGTQTAIEVPIIPLAQTAGANILLPRGPYNT- 183
Db 136 VLLGGKPIYANLKWSEEGFSIDVDDLOSKISKRTKMTVFNPHNPTGLFSPNDVKKI 195
QY 184 -RAAFNKLEVRHFLDPKQWEIIDSLESTADNTTAMWIINNNPCGVSVDHLAKV 242
Db 196 VDISRDNKILLSEIDYFNVEGKMRSTLSDSDWRFLIYVNGFSKTFSTNGWRLGYI- 254
QY 243 AEVARKLGIIVIADEVYKLVLSAPFIPMGVFGHIAPIVLSIGSLSKSVIIPGWRLGWA 302
Db 255 V-AKREIIQK--MGI-LAA--NVYTAPTSFVKRAVKAFD-TFDEV-NOMVSLFKRRDY 306
QY 303 VYDPTKILEKTKISTSIYINLVSTDPATFVQEAIPKILENTKADFFKRIIGLLKESSEI 362
Db 307 MYDELTKVKGVEVS-KPGAFYMPFNPNVSKILKTSFGDVKSIAKLIBEKGWVTIPGEVFP 365
QY 363 CYREIKENKTYTCPHKPGSGFMVVKLNLHLEIHDHDDFCCKLAKEESVILCPGVS-- 420
Db 366 LNICFEFLRLSFANVEEVKEGIQKIREF 394
QY 421 LGMEN-WVRITFACVPSSLDQGLERVKSF 448
RESULT 8
ENTRY #type complete
TITLE aspartate aminotransferase - Helicobacter pylori (strain J99)
ORGANISM #formal_name Helicobacter pylori
#variety strain J99
DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
05-Mar-1999
ACCESSIONS H71909
REFERENCE A71800
#authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.;
Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
```

```
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
G.F.; Trust, T.J.
Nature (1999) 397:176-180
Genomic sequence comparison of two unrelated isolates of the
human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession H71909
#status preliminary
#molecule_type DNA
#residues 1-390 #label ARN
#cross-references GB:AE001493; GB:AE001439; NID:g4155161; PID:g4155168
#experimental_source strain J99
GENETICS
#gene aspB
#superfamily aspartate transaminase
#length 390 #molecular-weight 42746 #checksum 4845
SUMMARY
Query Match 11.7%; Score 376; DB 2; Length 390;
Best Local Similarity 27.3%; Pred. No. 1.05e-43;
Matches 99; Conservative 83; Mismatches 158; Indels 23; Gaps 19;
Db 40 PDFTPQAIKDAAIKALNDG-FTKITPVAGIPPELLKATAFKLKKENNLDPSEILVSN 98
QY 92 PAFRTAVEADAVALRTGQFNCYRAGVGLPAARSAVAEHLQGVYKLSADSVFTLAG 151
Db 99 AKOSLFNAIQALI-GEQDEWIPVPFWTYPELVKYSQ-GVSQFIQTDEKSHFKITPKQL 156
QY 152 GQAEIVLIPVLAQTAGANILLPRGYPNYEARAAFNKLEVRHFLDPKQ-WEIDISL 210
Db 157 KDALSPK-TKMLILTPSNPTGMLYSKAELEALGEVLKDTKVWLSDEIYEKLVIY-KGEF 214
QY 211 -ESIADKNTTAMVIINPNPCGVSYSYDHLAKVAEVARKLGIIVIADEVYKLVLSAPF 269
Db 215 VSCAAVSEEMKRTITINGLSKSVAMTGRMGYAAKSKKLVKLMNSNQSOCTSNISIT 274
QY 270 IP-MGVFGHIA-PVLSIGLSKSVIIPGWRGVAVYDPTKILEKTKISTITNLVNST 327
Db 275 QMASIVALEGLVDKETMTRQAFKRC--HL-AHAKI--NAI-EG--LN-ALKPDGAFYL 325
QY 328 DPATFVQ-EAL-PKILENTKADFFKRIIGLLKESSEICVREIKENKTYTCPHKPGSMFV 385
Db 326 FNIIG-SLCGG--DSNRFCHELLEKEGVALVPGKAFLEGYVRLSFACSEIEKIGIRI 382
QY 386 MYKLNHLLEIHDHDDFCCKLAKEESVILCPGSLGVMENWVRITFACVPSSLDQGLERV 445
Db 383 ARF 385
QY 446 KSF 448
RESULT 9
ENTRY #type complete
TITLE hypothetical protein HP0672 - Helicobacter pylori (strain
26695)
ORGANISM #formal_name Helicobacter pylori
#variety strain J99
DATE 30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change
13-Sep-1998
ACCESSIONS H64603
REFERENCE A64520
#authors Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalakh, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
Helicobacter pylori.
```

```
#journal
#title
```

```
#cross-references MUID:96337999
#accession A64300
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-375 ##label BUL
#cross-references GB:U67459; GB:L77117; NID:g1590815; PID:g1592252;
TIGR:MJ0001; PID:g1510187

GENETICS
#map_position REV3343-2216
CLASSIFICATION #superfamily aspartate transaminase
KEYWORDS aminotransferase
SUMMARY #length 375 #molecular-weight 42395 #checksum 1390

Query Match 11.4%; Score 368; DB 2; Length 375;
Best Local Similarity 26.3%; Pred. No. 2.83e-42;
Matches 78; Conservative 84; Mismatches 117; Indels 18; Gaps 16;

Db 33 POFDTPKHIEAKRALDEKTH-YSPNNGIPELREISNKLKDDYNLQVDKNIIVTCG 91
QY 92 PAFRTAVEAEDAAALRTGQFCYAAGVGLPAARSAAVHLSQGVYKLSADDDVELTAG 151

Db 92 ASBALMSLMTLIDR-GDEVLIPNPFVSFTEPAEGKIKNIDL--DENFNIDLEKYK 148
QY 152 GTQAEVILPVLTAQTAGANILLPRPGYPNVEARAANKLEVRHFDLIPDKGEIDISL- 210

Db 149 ESIT-KTKLIIPNSPNTGKYDKETIKGLAEADYNLIIVSDVYDKIIYDKKHYS 207
QY 211 ESIADKNTTAMVIINPNPCGSYVSDHLAKVAEARKLILVIADEVYKGLVGSAPFI 270

Db 208 PMQ-FTDRC-IL-INGFSTYAMTGRIGLAYSDLNKELDLNNMIKHQY-SPAC-A 262
QY 271 PMGVGHIAPLVISIGLSKSWIPVGRGLGWAVYDP-TKILEKTKISTITNLYNVSTDP 329

Db 263 TTFAYQALAL-ALRGSQ-KCEDMVREFKMRDLIYNGLKDI-FKV--NKPDGAFYI 314
QY 330 AUFVQ-EALPKILENTKADFRRKIIGLLKESSEICYREIKENKIYTCPKHPSGMFV 385

RESULT 12
ENTRY #type complete
TITLE hypothetical protein Rv0858c - Mycobacterium tuberculosis
ORGANISM (strain H37Rv)
DATE #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
ACCESSION B70815
REFERENCE A70500
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmler, K.; Gas, S.; Barry III, C.E.; Rekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, K.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.

#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references MUID:98295987
#accession B70815
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-397 ##label COL
#cross-references GB:AL022004; GB:AL123456; NID:g3261550; PID:e1254000;
#experimental_source strain H37Rv

GENETICS
#gene Rv0858c
```

```
SUMMARY #length 397 #molecular-weight 42209 #checksum 1391

Query Match 11.2%; Score 361; DB 2; Length 397;
Best Local Similarity 30.9%; Pred. No. 5.00e-41;
Matches 68; Conservative 56; Mismatches 87; Indels 9; Gaps 9;

Db 57 YPPGGSAPLRRAIAAQRHRRHFGVDYD-PTEVLVTVGATEAIAAAVGLGVE-PGSEVLL 114
QY 116 YRAGVGLPAARSABA-EHLSQ-GVPYKLSADDDVFLTAGTQAEIVIPVLAQTAGANILL 173

Db 115 IEPFYDSYSPVAMAGAHRTVPLVDPGRGFDALDARAVTPTRTRALIINSPHNPTGA 174
QY 174 PRGYPNYEARAFAFNKLEVRHFDLIPD-KGEIDIDSLSESIADKNTTAMVIINPNPCGS 232

Db 175 VLSATELAIAEIAVAANLVLTDEVYEHVFDHARHPLAGDFGMAERTITISSAAKMF 234
QY 233 VYSYDHLAKVAEVARKLGIIVIADEVYKGLVGSAPFIPMGVFGHIA-PVLSIGSLSKSW 291

Db 235 NCTGMKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA 272
QY 292 IVPGRWLGWAVYDPTKILEKTKISTITNLYNVST-DFA 330

RESULT 13
ENTRY #type complete
TITLE aspartate transaminase (EC 2.6.1.1) - Bacillus sp. (strain YM-2)
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM #formal_name Bacillus sp.
DATE 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
ACCESSION A38621
REFERENCE A38621
#authors Sung, M.H.; Tanizawa, K.; Tanaka, H.; Kuramitsu, S.; Kegamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi, T.; Soda, K.
#journal J. Biol. Chem. (1991) 266:2567-2572
#title Thermostable aspartate aminotransferase from a thermophilic Bacillus species. Gene cloning, sequence determination, and preliminary X-ray characterization.
#cross-references MUID:91115885
#accession A38621
#status preliminary
#molecule_type DNA
#residues 1-392 ##label SUN
#cross-references GB:M59430; NID:g142537; PID:g142538
CLASSIFICATION #superfamily aspartate transaminase
KEYWORDS aminotransferase
SUMMARY #length 392 #molecular-weight 42661 #checksum 7039

Query Match 11.1%; Score 358; DB 2; Length 392;
Best Local Similarity 23.5%; Pred. No. 1.71e-40;
Matches 85; Conservative 105; Mismatches 154; Indels 18; Gaps 17;

Db 42 PDFNTPQNMDAIDSMOOG-YTKYTPSGGLPALKQAIIERKRDQNLQYKPEIIVGVG 100
QY 92 PAFRTAVEAEDAAALRTGQFCYAAGVGLPAARSAAVHLSQGVYKLSADDDVELTAG 151

Db 101 AKHVLYTLFQVILN-EGDEVILPIPYWVSYPEQVKLAG-GYPVYIEATSEQNYKTAQL 158
QY 152 GTQAEVILPVLTAQTAGANILLPRPGYPNVEARAFAFNKLEVRHF-DLIPDKGEIDISL 210

Db 159 KNAITDK-TKAVIINSPNPTGMVYTRREEDIAKIALENLIVSDIYEKLNGAEH 217
QY 211 -ESIADKNTTAMVIINPNPCGSYVSDHLAKVAEARKLILVIADEVYKGLV-LSAP 268

Db 218 FSIQISBEVKAQIVINGVSKSHMTGWRIGYAG-NADIINAMTDLASHSTSNPTTAS 276
QY 269 FIPMGVFGHI-APVLSIGSLSKSWIPVGRWLGWAVYDPTKILEKTKISTITNLYNVST 327

Db 277 QYAA-I-EAY-NGPQDSVEEMRKAFESRL-ET--I-YPKLSAIPGKVV-KPOGAFYLLP 328
QY 328 DPATFVQALPKILENTKADFRRKIIGLLKESSEICYREIKENKIYTCPKHPSGMFV 387
```



```

Db 329 DYSEAAQKGFASVDFEAFALLTEANVAVIPGSGFAPSTIRISVATSLNLTEAERID 388
QY 388 KLNHLLEIEHDDID-FCCKLAKEESVILCPGSLVGMENWRLTFACVPSSLODGLERYK 446
Db 389 RF 390
QY 447 SF 448

RESULT 14
ENTRY
TITLE #type complete
ORGANISM #formal_name Pyrococcus horikoshii
DATE 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
E71125
ACCESSIONS
REFERENCE #authors
Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
#journal DNA Res. (1998) 5:55-76
#title Complete sequence and gene organization of the genome of a
hyper-thermophilic archaeobacterium, Pyrococcus horikoshii
OT3.
#cross-references MUID:98344137
#accession E71125
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-391 #label KAW
#cross-references GB:AF000003; NID:g3236130; PID:d1030806; PID:g3257180
#experimental_source strain OT3
#note this accession replaces an interim accession for a
sequence replaced by GenBank

GENETICS
#gene PH0771
SUMMARY #length 391 #molecular-weight 44565 #checksum 193
Query Match 10.2%; Score 330; DB 2; Length 391;
Best Local Similarity 28.4%; Pred. No. 1.50e-35;
Matches 103; Conservative 82; Mismatches 148; Indels 30; Gaps 29;

Db 42 PDFTPKNIKAARALDEG-WHYHTNAGIPELREAVVEYKKFYGIDIEVENVIITAG 100
QY 92 PAFRTAVEAEDAVAAALRTGQFCNCTAAGVGLPAARSAVAEHLSSQGVPKLSADDFLTAG 151
Db 101 AYECTYLAFFESLLER-GDEVIIPDPFVSVAEDAERAK-PVR-IPLRENNFLPPNE 157
QY 152 GTQAEVVIIPVLAQTAGANILLPRGPVNY-E-ARAFNKLEVRHFDLIPDKGWEIDIDS 209
Db 158 LLEKIS-KNTR-MIVINYPNNTGATLD-KELAKTIADIAEDYNIYILSDPEYHFHYED 214
QY 210 L-ESIADKNNTAMVIIN-PNPNCGSVSYSDHLAK-VAEVARKLGIIVTADEVYKLVLS 266
Db 215 AKHPYMKTKAPENTILA-NSFSKTFMTGWRGLFV-V-APSOVI-K-EM-TKLHAYV-IG 267
QY 267 APFIPMGVFGHIAFVLSIGSLGSWIPGWRGLGWVAVDYDPTKILEKTKISTSIYNIYNVS 326
Db 268 -NVASFVQIAGIEAL-RS-EESWKAVEREMKKEYNERRKIVVVKRLKNMPPGIVKPKPGAFY 324
QY 327 TDPATFVQEALPKILENTKADFFRIIGLLKESSEICVREIKENYITCPH-K-PEGSMF 384
Db 325 VFPNIS-G--TGMSE-KFSEWLLKARVVPVPGTAFGRMGEGVYRVSATSKLETEAM 380
QY 385 VMVKLNHLLEIHHDDIDFCCKLAKEESVILCPGSLVGM-ENWVRITFACVPSSLODGL 442
Db 381 NRI 383
QY 381 NRI 383

```

QY 443 ERV 445

RESULT 15

ENTRY #type complete

TITLE #formal\_name Bacillus subtilis

ORGANISM #formal\_name Bacillus subtilis

DATE 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change

ACCESSIONS

REFERENCE #authors

Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;

Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;

Biolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,

A.; Braun, M.; Brigneau, S.C.; Bron, S.; Brouillet, S.;

Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;

Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;

Enright, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;

Fabret, C.; Ferrarri, E.; Foulger, D.; Fritz, C.; Fujita,

M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,

S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;

Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,

C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;

Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;

Kasahara, Y.; Klaer-Blanchard, M.; Klein, C.; Kobayashi,

Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.;

Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;

Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;

Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,

M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,

V.; Pohl, T.M.; Portetelle, D.; Porwollik, S.; Prescott, G.;

A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, E.;

Rev, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;

Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;

Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;

Sekowska, A.; Seror, S.J.; Serrot, P.; Shin, B.S.; Soldo,

B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takanashi, H.;

Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;

Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;

Vandenbol, M.; Vannier, F.; Vassarotti, C.; Viari, A.;

Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.;

Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,

K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.;

Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256

#title The complete genome sequence of the Gram-positive bacterium

#accession Bacillus subtilis.

#cross-references MUID:98044033

#status preliminary; nucleic acid sequence not shown;

#molecule\_type DNA

#residues 1-393 #label KUN

#cross-references GB:299115; GB:AL009126; NID:g2634478; PID:el183682;

PID:g2634655

#experimental\_source strain 168

GENETICS

#gene aspb

CLASSIFICATION

SUMMARY #superfamily aspartate transaminase

#length 393 #molecular-weight 43088 #checksum 6856

Query Match 10.2%; Score 330; DB 2; Length 393;

Best Local Similarity 23.2%; Pred. No. 1.50e-35;

Matches 85; Conservative 117; Mismatches 145; Indels 20; Gaps 18;

Db 40 PDFTPHIIDAARVSNNEGHTR-YTPSGGLAEKKNIAEKKRDNIEYK-PSQ-IIIVC 96

QY 92 PAFRTAVEAEDAVAAALRTGQFCNCTAAGVGLPAARSAVAEHL--SQGVPKLSADDFLT 149

Db 97 TGAKHALYTLFQVILD-EEDVVIPTPYWYSYPEQVQKAGGKPVYEGLENNHFKISPEQ 155

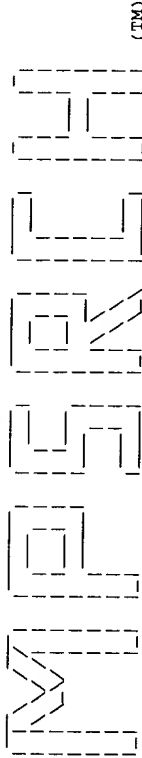


QY 150 AGTQAEVPIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDS 209  
Db 156 LKNAITEK-TKAIVINSPSNPTGVMYTEELSALGEVLEHDILIVSDEIYEKLYGGKK 214  
QY 210 L-ESIAKNTTAMVIINPNPCGSVSYDHLAKVAEVARKLGLIIVIADEVYKLVLSAP 268  
Db 215 HYSIAQLSDRLXEOTVIINGVSKSHSMTGWRIGYAA--GSEDII-KA-M-TNLASH-STS 268  
QY 269 FIPMGVFG-HI-APVLSIGLSKSWIVPGWRIGWVAVYDPTKILEKTKISTITNYLNVS 326  
Db 269 -NPTSLAQYG-AIAAYNGSPSEPLEEMREAFEHRLNTIYAKLIEIPGFSCV-KPEGAFYLF 325  
QY 327 TDPAFVQEQALPKILENTRKADFCKRIIGLLKESSEICYEIKENKYITCPHKPEGSMFVM 386  
Db 326 PNAKEAAQSCGKVDVFKALLEEKVAIVPGSGFGSPENWRISYATSLDLEAEIERI 385  
QY 387 VKLNLHLE-EIHDDIDFCCKLAKEESVILCFGSVIGMENWVRITFACVPSSLQDGLERV 445  
Db 386 KREVEKH 392  
QY 446 KSFQORN 452

Search completed: Fri Oct 1 13:52:21 1999  
Job time : 28 secs.



\*\*\*\*\*



\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:50:18 1999; MasPar time 15.42 Seconds

Tabular output not generated. 844.953 Million cell updates/sec

Title: >US-09-026-400-2  
Description: (1-461) from US09026400.pap  
Perfect Score: 3223  
Sequence: 1 MVHQSNHGGEAAAAANGKS.....LERVKSFQRNKKNSINGC 461

Scoring table: PAM 150  
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot37  
1:swissprot

Statistics: Mean 51.018; Variance 91.346; scale 0.559

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	920	28.5	1	ATY_HUMAN	3.49e-173
2	914	28.4	1	ATY_HUMAN	8.32e-172
3	570	17.7	416	TYR_TYR	5.46e-94
4	394	12.2	401	AAT_SULSO	1.09e-55
5	368	11.4	375	ASPARTATE AMINOTRANSFERASE	3.41e-50
6	358	11.1	392	PUTATIVE ASPARTATE AMINOTRANSFERASE	4.28e-48
7	345	10.7	393	ASPARTATE AMINOTRANSFERASE	2.22e-45
8	330	10.2	393	ASPARTATE AMINOTRANSFERASE	2.86e-42
9	301	9.3	392	PUTATIVE AMINOTRANSFERASE	2.51e-36
10	300	9.3	592	PUTATIVE AMINOTRANSFERASE	4.00e-36
11	294	9.1	507	PUTATIVE ALANINE AMINO	6.58e-35
12	285	8.8	400	PUTATIVE AMINOTRANSFERASE	4.29e-33
13	258	8.0	444	YU00_YEAST	1.01e-27
14	255	7.9	505	PUTATIVE ALANINE AMINO	3.91e-27
15	241	7.5	410	ATAT_SCHPO	2.09e-24
16	243	7.5	421	ATAT_RHIME	8.56e-25
17	235	7.3	386	YB0L_ECOLI	3.00e-23
18	231	7.2	482	AL02_HORVU	1.75e-22
19	222	6.9	387	PATB_BACSU	9.06e-21
20	221	6.9	399	PATB_BACSU	1.40e-20
21	222	6.9	517	IAIC_DIACA	9.06e-20
22	217	6.7	482	AL02_PANMI	7.96e-20
23	211	6.5	213	AAT_STRGR	1.06e-18



[illegible]

```

RESULT      5
AC    AATL1-METJA          STANDARD;             PRT;       375 AA.
AD    Q60317;
AI    01-NOV-1997 (REL. 35, CREATED)
DT    01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DI    01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE    PUTATIVE ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE A)
DE    (ASPART).
DN    MJ0001.
OS    METHANOCOCCUS JANNASCHII.
OC    ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
OC    METHANOCOCCUS.
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX    MEDLINE; 96337999.
RA    BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA    SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCCAYNE J.D.,
RA    KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA    OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEX A.,
RA    SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA    UTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA    COTTON M.D., ROBERTS K.M., HORST M.A., KAINE B.P., BORODOVSKIY M.,
RA    KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT    *Complete genome sequence of the methanogenic archaeon, Methanococcus
RT    jannaschii.*;
RL    SCIENCE 273:1058-1073(1996).
CC    -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC    L-GLUTAMATE (BY SIMILARITY).
CC    -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC    CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC    AMINOTRANSFERASES.
-----
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
-----
CC    EMBL; U67459; G1592252; -.
CC    TIGR; MJ0001; -.
DR    PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR    PFAM; PF00155; aminotran_1; 1.
KW    TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT    BINDING 223 223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ    SEQUENCE 375 AA; 42395 MW; 166A9EFC CRC32;
Query Match 11.4%; Score 368; DB 1; Length 375;
Best Local Similarity 26.3%; Pred. No. 3,41e-50;
Matches 78; Conservative
Db 33 PDFTPDKHIEAAKRALDGKTH-YSPNNGIPELFEEISLNKKDDYNLDVDKDNIVTCG 91
Qy 92 PAFRVAVEADAVALATGTGFNCYAAGVGIPAAARSVAEHLSQGPYKLSDADVFLTAG 151
Db 92 ASEALLMSITLIIDR-GDEVLPINPSFYVSFTSLTEFAEGTKNIDL--DENFNIDLEKVK 148
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

QY	152	GTQIAEVIIPVLAQTAGANILLPRPGYPNPYEARAANKLEVRHFDLIPKQWEIDTDSL-	210
Db	149	ESIT-KTKTILIFNSPNSCKYVDKETIKGLAEIAEDYNLIIVSEVDKIIYDKKHS	207
QY	211	ESIAADKNTTAMWIINPNPCGSVSYSDHLAKVAEVARKEILVIADEVTKLVLSAPFI	270
Db	208	PMQ-FTDRC-IL-INGFSKYTYMTGWRIGYLVASDELNKELDILNNMKIKHY-SFAC-A	262
QY	271	PMGVFGHIAPVLISGSLSKSWIIPVGRLGMVAVDP-TKILEKTKISTITNVLNVSTDP	329
Db	263	TTFAQYGALA-ALRGSQ-KCEDWDEAFKMRRLDIYNGLKDI-FKV-NKPDGAYVI	314
QY	330	ATFVQ-EALPKILIENTKADFRIIGLLKSSICREYIKENKIYITCPHSGSFMFV	385

RESULT	6	STANDARD;	PRT;	392 AA.
ID	AAT_BACSP			
AC	P23034;			
DT	01-NOV-1991 (REL. 20, CREATED)			
DT	01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).			
OS	BACILLUS SP. (STRAIN IM-2).			
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;			
OC	BACILLUS.			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE; 91115885.			
RA	SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,			
RA	HIRONOBU K., OKAMOTO A., HIGUCHI T., SODA K.;			
RT	"Thermostable aspartate aminotransferase from a thermophilic Bacillus			
RT	species. Gene cloning, sequence determination, and preliminary X-ray			
RT	characterization."			
RL	J. BIOL. CHEM. 266:2567-2572(1991).			

[2]  
SEQUENCE OF 1-24 AND 387-392.  
RX MEDLINE: 90170846.  
RA SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,  
SODA K.,  
RT "Purification and characterization of thermostable aspartate  
amino transferase from a thermophilic Bacillus species.";  
RL J. BACTERIOL. 172:1345-1351(1990).  
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLOUTARATE = OXALOACETATE +  
L-GLUTAMATE.  
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS.  
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
AMINOTRANSFERASES.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collabora-  
CC tion between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC at the European Bioinformatics Institute. There are no restrictions on  
CC use by non-profit institutions as long as its content is in no  
CC modified and this statement is not removed, usage by and for commer-  
CC cial entities requires a license agreement (See <http://www.isb-sib.ch/announc>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

CC      EMBL; M59430; G142538; -
DR      PIR; A38621; A38621.
DR      PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR      PFAM; PF00155; aminotran_1; 1.
KW      TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT      BINDING 239 239 PYRIDOXAL PHOSPHATE.
FT      CONFLICT 338 388 D -> L (IN REF. 2).
SQ      SEQUENCE 392 AA; 42661 MW; 8F0EC6D0 CRC32;

Query Match      11.1%; Score 358; DB 1; Length 392;
Best Local Similarity 23.5%; Pred.No. 4.28e-48;
Matches 85; Conservative 105; Mismatches 154; Indels 18; Gaps 1

```

D<sub>b</sub> 42 PDFTPQNTMDAAIDSMQQG-YTKYTPSGGLPALKQAIIEKFRDNQLEYKPNIEIVGVG 100  
| | | : | | : : | : : | | | : | : : : : : |

Qy	92	P A F T A V E A D A V A A L R T G O F N C Y A A G V G P A A R S A V A E H L S Q G V P Y K L S A D D V F I T A G	151
D b	101	A K H Y L Y L F Q V I L N - E G D E V I I P I Y W S Y P E O V K L A G - G V P Y V I E A T S Q N Y K I I A E Q L	158
Q y	152	G T Q A E I V I P V I A Q T A G A N I L L P R P G P V N T E A R A F N K L E R H F - D U I P D K G W E I D I S L	210
D b	159	K N A I T D K - T R A V I I N S P N P T G M V Y T R E E L E D I A K L A E N N I I L V S D E I Y E K L I Y N G A E H	217
Q y	211	- E S I A D K N T T A M V I I N P N P C G S V S Y D H L A K V A E A R K G I L V I A D E V Y G K L V L - G S A P	268
D b	218	F S I A Q I E E V K A Q T I V I N G Y S K S H S M T G W I G I Y A A G - N A D I I N A M T D L A S H S T S N P T T A S	276
Q y	269	F I P M G V F G H I - A P V L S I G S L S K S I W I P B G L W G V A V D P T K I L E K T K I S T S I T N Y L N V S T	327
D b	277	Q Y A A - I - E A Y - N G P Q D S V E E M R K A F E S R L - E T - I - Y P K L S A T P G K V V - K P O G A Y P L P	328
Q y	328	D P A T F V O A L P K I L E N T K A O F F K R I I G L L K E S S E I C Y R E I K E N Y I T C P H K P E G S F M V M	387
D b	329	D V S E A A Q K T F A S D E F A S A L L T E A N V A V P G G F G A P S T I R I S Y A T S L N L I E A T E R I D	388
Q y	388	K I N L H L L E E T H D D I D - F C C K L A K E E S V I L C P G S V L G M E N W N R I T F A C V P S S Q D G L E R V K	446
D b	389	R F 390	
Q y	447	S F 448	

RESULT		7				
ID	AAT	BACST	STANDARD;	PRT;	393	AA.
AC	Q59228;					
DT	01-NOV-1997	(REL. 35,	CREATED)			
DT	01-NOV-1997	(REL. 35,	LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35,	LAST ANNOTATION UPDATE)			
DE	ASPARTATE AMINOTRANSFERASE	(EC 2.6.1.1) {TRANSAMINASE A} (ASPAT).				
GN	ASPC.					
OS	BACILLUS STEAROTHERMOPHILUS.					
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;					
QC	BACILLUS.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=ATCC 12980;					
RX	MEDLINE; 96434469.					
RA	BARTSCH K., SCHNEIDER R., SCHULZ A.;					
RT	"Stereospecific production of the herbicide phosphinothricin					
RT	(glufosinate): purification of aspartate transaminase from Bacillus					
RT	scaerothermophilus, cloning of the corresponding gene, aspC, and					
RT	application in a coupled transaminase process.;"					
RL	APPL. ENVIRON. MICROBIOL. 62:3794-3799(1996).					
CC	-1- CATALYTIC ACTIVITY: L-ASPARTE + 2-OXOGLUUTARATE - OXALOACETATE +					
CC	L-GLUTAMATE.					
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.					
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).					
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT					
CC	AMINOTRANSFERASES.					

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X93600; E212847; -  
DR PROSITE: PSQ0105; AA\_TRANSFER\_CLASS\_1; 1.  
DR PFAM: PF00155; amino\_tran\_1; 1.  
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.  
FT BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

Query Match 10.7%; Score 345; DB 1; Length 393;  
Best Local Similarity 23.8%; Pred. No. 2.22e-45;  
Matches 86; Conservative 104; Mismatches 154; Indels





[illegible]

QY 78 RPVLPLAHGDPSPVFPFPAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLTSQGV 137

DB 86 NLDYTA AQITV GIGKQILFN AFMAILN - FGDEVVIFAF INWSTIEFENVATCS QIATV 142

THE UNIVERSITY OF CHICAGO

[illegible]

24 200MVEHT MYCDERELTDIEVERDCTYEPRTI TMNCVSKAVAMTGWRTGYAA--GPI.H-I.TK 259

255 ADEVYGKLVLSAPF-IPMGV-FGHIAPVLSIGLSKSWIVPGWRLGWAVYDPTKILEK 312

D<sub>b</sub> 260 A-MDM-IQG-QQTS-GAASIAQWAAVEALNGPQ-DFIGNKEIFQGRDLVVSMLNQAKG 314

**THE UNIVERSITY OF CHICAGO PRESS**

373 ITCPBHKDECSMEVAM/K - I NL -- HIJ -- FF - THDDIDECKTAKESVTLCPGSVLGMENW 426

Db 374 FRISYATSEALLEEACRRIORFC 396

QY 427 VRITFACVPSSLQDGLERVKSFC 449

ID IUGV\_FIRST STANDARD, 111 1111  
AC P47039:

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DE HYPOTHETICAL AMINOTRANSFERASE YJL060W (EC 2.6.1.1.-).

US SACCHAROMYCES CEREVISIAE (BAKER & LEAST).  
OC EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES: SACCHAROMYCETALES:

RN [1]

RA POHL T.M., ALJINOVIC G.;

RN [2]  
SEQUENCE OF 02-222 FROM N A

RX MEDLINE: 95400292.

RA SASANUMA S., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,

### RT "Analysis of the nucleotide sequence of chromosome VI from

RT NAL: GENEL: 10:201 200(1955):  
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).

CC AMINOTRANSFERASES.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration with the EMBL Data Bank and the EMBL Outstation at the EMBL Laboratory of Molecular Biology and the EMBL Outstation at the EMBL Laboratory of Molecular Biology.

use by non-profit institutions as long as its content is in no

CC entities requires a license agreement (See <http://www.isb-sib.ch/announc>

22

DR EMBL; D44603; G871966; - .  
DB PROSITE: PS00105: AA TRANSFER CLASS 1: 1

**VPC**

KW HYPOTHETICAL PROTEIN; AMINOTRANSFERASE; TRANSFERASE;  
 KW PYRIDOXAL PHOSPHATE.  
 FT BINDING 271 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 444 AA; 50082 MW; 16A5EF3D CRC32;

Query Match 8.0%; Score 258; DB 1; Length 444;  
 Best Local Similarity 32.7%; Pred. No. 1.01e-27;  
 Matches 33; Conservative 32; Mismatches 33; Indels 3; Gaps 3;

Db 184 WTIDFQEFKATSKTAVINTPHNPVFTRELLTIGNICVKNHVVISDEYVHL 243  
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
 QY 203 WEIDDSLESIAKNTAMVILNPNPCGVSVDYDLAKVAEVRKLGILVIADEVYGL 262  
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
 Db 244 YF-TDSTRIATLSPEIGQTLTVGSGAGKSAATGWRIGWV 283  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 QY 263 VLGSAPPFPMGVFG-HIAPV-LSIGSLSKSWIYPGWRGLGWV 301  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14  
 ID ALAT\_SCHPO STANDARD; PRT; 505 AA.  
 AC Q10334;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE PUTATIVE ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC  
 DE TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).  
 GN SPAC19G10.04C.  
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;  
 OC SCHIZOSACCHAROMYCETEALES; SCHIZOSACCHAROMYCETACEAE;  
 OC SCHIZOSACCHAROMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;  
 RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -!- CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLUTARATE -> PYRUVATE +  
 CC L-GLUTAMATE.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 CC -!- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; E225673; -.  
 DR PFAM; PF00155; aminotran\_1; 1.  
 DR KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;  
 FT BINDING 326 326 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 505 AA; 56627 MW; 8CD487CF CRC32;

Query Match 7.9%; Score 255; DB 1; Length 505;  
 Best Local Similarity 28.6%; Pred. No. 3.91e-27;  
 Matches 54; Conservative 49; Mismatches 75; Indels 11; Gaps 10;

Db 100 PTL-LDHAEEKWFLNPTDVFORS-KMLLKESGSLGAYSASOGIPLVRHVADFTIR 156  
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
 QY 79 PVLPLANGDPVFFPA-FRTAVEADAVAAALR-TGQNCYAAAGVLGPAARSVAEHL 136  
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
 Db 157 DGFQCEPSDIYLTSGASHAARLIMTLIARTDGMVPAFQYPLYGAIQIDLMGSMVYS 216  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 QY 137 VPKLSADDFVLTAGGTOAIEVITPVLQAOTAGANILLPRGYPNYEARAAFNKLEVRHF 196  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 Db 217 LSENNWDIDDFQKKSDFDEASKGINVRLCVINPNCPTGACISENSEKVLRFKAGK 276  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 QY 197 LIPDKGWEIDDSLE-SDAD--KN-TTA-M-VIINPNPCGVSVDYDLAKVAEVRKLG 250  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Db 277 IVLIADEVY 285  
 | : : | | | | |  
 QY 251 IVLIADEVY 259

RESULT 15  
 ID AATBE\_RHIME STANDARD; PRT; 410 AA.  
 AC Q06191;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE ASPARTATE AMINOTRANSFERASE B (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).  
 GN AATBE.  
 OS RHIZOBIUM MELLIOTI.  
 OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;  
 OC RHIZOBIACEAE; SINORHIZOBIUM.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-104A14;  
 RX MEDLINE; 93308098.  
 RA ALFANO J.R., KAHN M.L.;  
 RT "Isolation and characterization of a gene coding for a novel  
 RT aspartate aminotransferase from Rhizobium meliloti.";  
 RL J. BACTERIOL. 175:4186-4196(1993).  
 CC -!- FUNCTION: INVOLVED IN SYMBIOTIC NITROGEN FIXATION.  
 CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE -> OXALOACETATE +  
 CC L-GLUTAMATE.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L12149; G152151; -.  
 DR PIR; A40658; A40658  
 DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 DR PFAM; PF00155; aminotran\_1; 1.  
 KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.  
 FT BINDING 249 249 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 410 AA; 44453 MW; C72D06D6 CRC32;

Query Match 7.5%; Score 241; DB 1; Length 410;  
 Best Local Similarity 21.0%; Pred. No. 2.09e-24;  
 Matches 77; Conservative 100; Mismatches 174; Indels 16; Gaps 15;

Db 51 PDFDTPDHVKQAASDAIHRGETK-YTALDGTPELKKAIREKFEQRENGLAYEL--DEITVA 107  
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 QY 92 PAFRTAVEADAVAAALRTGQNCYAAAGVGLPAARSVAEHL-SQ-GVPYKLSADDFVLT 149  
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 108 TCAGKILFNAMMASL-D-PGDEVVITPTWTYSYSDIVQICEGKPIILLIACDASSGFRLTAQ 165  
 : | : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :  
 QY 150 AGGTOAI-EVIIPVLAQTAGANILLPRGYPNYEARAAFNKLEVRHFDLIPDKGWEID 208  
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 166 KLEAAITPTRTWVLLNSPNSPAGAAVSADYRPLDVLKHPHVVLLVDDMYEHIVYDAF 225  
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 QY 209 SLESIAKNTTAMVILNPNPCGVSVDYDLAKVAEVRKLG-ILVIADEVYGLVLSA 267  
 | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 226 RVVTPARLEPGLKDRTLTVNGSKAYAMTGNRIGVAGG-PRALIKAMAVQSAQSCPS 284  
 : | : | : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :  
 QY 268 PPI-PMGV-FGHIAVLSIGLSKSWIYPGWRGLGWAVVDPDKLEKTKISTSTINLVN 325  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 Db 285 VSOAAASVAALNGPODFLKERTESFORRNVLVNGLNA-IEGL-DCRVPEGAFTFPGCAG 342  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 QY 326 STDPTATFVQEAALPKILENTKADFFKRIITGLKESSEICYREIKENKYYITCP-HKPEGS 384  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
 Db 343 VARRVTPSG-KRIESDTDFCAYLLEDSHVAVVPGSAFGLSPYFRISYATSEALKEALR 401  
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 385 VVVKLNHLLEEHDDIDECCKLAKESVILCPGSLGMENWVRITFACVPSSLQDGLER 444  
Db 402 ISAACKR 408  
QY 445 VKSFCOR 451

Search completed: Fri Oct 1 13:50:38 1999  
Job time : 20 secs.